

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: December 30, 2005, 09:36:25 ; Search time 2698 Seconds
(without alignments)
18724.377 Million cell updates/sec

Title: US-10-650-249-1
Perfect score: 7580
Sequence: 1 agctctattatcaagaga.....gccgcaccgcggtggagct 7580

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0
Searched: 4996997 seqs, 332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004as.*
13: geneseqn2004bs.*
14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7580	100.0	7580	12	ADL71829 Arabidops
2	1730	22.8	1746	12	ADL71846 Arabidops
3	1402.4	18.5	10078	6	ABQ73047 Tomato an
4	1367.4	18.0	17511	14	ADV39061 Plant gen
5	1367.4	18.0	18987	14	ADV39062 Plant gen
6	1360	17.9	1361	3	AA88401 4x Camv 3
7	1235	16.3	1235	12	ADL71845 Arabidops
8	1062	14.0	1062	12	ADL71848 Arabidops
9	1058	14.0	1058	12	ADL71847 Arabidops
10	888	11.7	888	12	ADL71840 Arabidops
11	692	9.1	795	10	ADD30377 Plant yie
12	692	9.1	795	12	ADL44304 Plant tra
13	684	9.0	684	12	ADL71843 Arabidops
14	621	8.2	5033	2	AAQ74695 pPHI1406
15	617.2	8.1	4727	14	AEA40942 T-DNA reg
16	617.2	8.1	8428	8	ABT16592 Artificia
17	617.2	8.1	8428	8	ACC44694 Plasmid p
18	617.2	8.1	10122	8	ABT16598 Artificia
19	617.2	8.1	10122	10	ACC44701 Plasmid p

20	617.2	8.1	10549	8	ABT16593 Artificia
21	617.2	8.1	10549	10	ACC44696 Plasmid p
22	617.2	8.1	11182	8	ABT16591 Artificia
23	617.2	8.1	11182	10	ACC44693 Vector pA
24	617.2	8.1	11478	8	ABV75873 Vector pP
25	617.2	8.1	11667	10	ADH89347 Suppressi
26	617.2	8.1	12304	8	ABV75876 Luciferas
27	617.2	8.1	12368	13	ADV16236 Planc tra
28	617.2	8.1	12497	8	ABV75875
29	617.2	8.1	12592	8	ABT16596 Artificia
30	617.2	8.1	12592	10	ACC44699 Vector pA
31	617.2	8.1	12614	4	AAC66931 Plant eig
32	617.2	8.1	12921	3	AAA97523 Plasmid p
33	617.2	8.1	14627	8	ABT16610 Artificia
34	617.2	8.1	14627	10	ACC44712 Plasmid p
35	616.8	8.1	829	4	AAF81265 Cauliflow
36	616.8	8.1	829	9	ADA44822 Cauliflow
37	615	8.1	5475	8	ABV75872 Vector pT
38	614.6	8.1	1334	2	AAZ27627 Plasmid S
39	612.8	8.1	5013	14	AEA40941 T-DNA reg
40	612	8.1	4727	14	AEA40942 T-DNA reg
41	611.8	8.1	1216	8	ABV75874 Plant vec
42	610.6	8.1	781	14	AEA28179 Alfalfa m
43	610.6	8.1	781	14	AEA33917 CamV 35S
44	599.6	7.9	11182	8	ABT16591 Artificia
45	599.6	7.9	11182	10	ACC44693 Vector pA

ALIGNMENTS

RESULT 1
ADL71829
ID ADL71829 standard; DNA; 7580 BP.
XX
AC ADL71829;
XX
DT 20-MAY-2004 (first entry)
XX
DE Arabidopsis thaliana OBP3 DNA.
XX
KW Transgenic plant; Dof transcription factor; ocs binding factor;
KW plant size; plant stature; root growth; plant; gene; ds; OBF;
KW OBF binding protein; OBP3; SOB1; mouse-ear cross.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 4103..5119
FT /*tag= a
FT /product= "Arabidopsis thaliana OBP3 protein"
FT /transl_except= (pos:4811..4909, aa:Gly-Gly)
XX
PN US2004045055-A1.
PD 04-MAR-2004.
PP 28-AUG-2003; 2003US-00650249.
XX
XX 28-AUG-2002; 2002US-0406657P.
PR (UNIW) UNIV WASHINGTON.
PI Neff MM;
XX WPI; 2004-225757/21.
DR P-PSDB; ADL71830.
PT New transgenic plant cell, useful in producing plants with altered size
PT and stature and with normal and healthy root growth.
XX Claim 24; SEQ ID NO 1; 53pp; English.
XX

CC The invention relates to a transgenic plant transformed by a Dof
CC transcription factor, OBF (ocs binding factor) binding protein (OBP3).
CC OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic
CC acid and polypeptides are useful in producing transgenic plants with
CC altered size and stature and with normal and healthy root growth. The
CC present sequence is Arabidopsis thaliana OBP3 DNA.
XX
SQ Sequence 7580 BP; 2376 A; 1376 C; 1291 G; 2537 T; 0 U; 0 Other;
Query Match 100.0%; Score 7580; DB 12; Length 7580;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTCTATTAAATTCAGAGAGAGAGCAAAATAAGAGCAAAAACTCAAAACCTTAAGTTTCTGA 60
DB 1 AGCTCTATTAAATTCAGAGAGAGAGCAAAATAAGAGCAAAAACTCAAAACCTTAAGTTTCTGA 60
QY 61 ATATGAAGGGGTAGATAATCATCTCTCAACTAGTTTAAAAAAGTATGATAAAATTA 120
DB 61 ATATGAAGGGGTAGATAATCATCTCTCAACTAGTTTAAAAAAGTATGATAAAATTA 120
QY 121 AAAACACAATGGATCAATTAAGAGACAGTAGTTTATGATATATATATGTTGGGATCGATTA 180
DB 121 AAAACACAATGGATCAATTAAGAGACAGTAGTTTATGATATATATATGTTGGGATCGATTA 180
QY 181 GTTGACATCAAAAGATCAAAATATGACCGGTAAATGCGCAAAATACCAAGGCGCAATT 240
DB 181 GTTGACATCAAAAGATCAAAATATGACCGGTAAATGCGCAAAATACCAAGGCGCAATT 240
QY 241 CATGGATATCAAAACACCTTAATGTCATTCAAATCTATACTAACTACTATCTCAATTA 300
DB 241 CATGGATATCAAAACACCTTAATGTCATTCAAATCTATACTAACTACTATCTCAATTA 300
QY 301 CAAAGCTAGTAGATTTTCTCAAAGTGAGCAACAGTCTAATTTCTCGAAAAAATCTGTT 360
DB 301 CAAAGCTAGTAGATTTTCTCAAAGTGAGCAACAGTCTAATTTCTCGAAAAAATCTGTT 360
QY 361 TTTTCCGAGTAAATATCAATCTACTTACTA CAATTTGAGCAATTAATCTAGTTTCT 420
DB 361 TTTTCCGAGTAAATATCAATCTACTTACTA CAATTTGAGCAATTAATCTAGTTTCT 420
QY 421 CTGCACTTTAAACACAGGTGTACAGTGTCAACACAGATCTAGGTTAAACACCTTAAG 480
DB 421 CTGCACTTTAAACACAGGTGTACAGTGTCAACACAGATCTAGGTTAAACACCTTAAG 480
QY 481 CTAGTACTTAAATAGATATGCTATTTTTCGACCATTTATATATATATATATATATAT 540
DB 481 CTAGTACTTAAATAGATATGCTATTTTTCGACCATTTATATATATATATATATATAT 540
QY 541 TTCGTGAAAAATGCGCATGTTCTTGTGGAACTTAGGAATCTTCTTACTAAAGATTG 600
DB 541 TTCGTGAAAAATGCGCATGTTCTTGTGGAACTTAGGAATCTTCTTACTAAAGATTG 600
QY 601 GCATGACCGTGTAAACGATTTCCATGTACTATCTCGATATTTTCCACACCTTAATAT 660
DB 601 GCATGACCGTGTAAACGATTTCCATGTACTATCTCGATATTTTCCACACCTTAATAT 660
QY 661 CTTGAAAAATTAAGATCAAAATATATGAGAACATATATTTGATCATTTGTTAAATAGCCT 720
DB 661 CTTGAAAAATTAAGATCAAAATATATGAGAACATATATTTGATCATTTGTTAAATAGCCT 720
QY 721 TATATAGTGTAGATGTGAACCTATGAGATCAAAAAAATAAGGAAAGAAAGCTGCGAG 780
DB 721 TATATAGTGTAGATGTGAACCTATGAGATCAAAAAAATAAGGAAAGAAAGCTGCGAG 780
QY 781 AGAAGGTGTGCTTTTCAACTATGAATATGGGCTCATGAGATGTACACTACAGATAAGCG 840
DB 781 AGAAGGTGTGCTTTTCAACTATGAATATGGGCTCATGAGATGTACACTACAGATAAGCG 840
QY 841 AAGATTTCTGTGTCATGAAAAATGTGTACTTAATAAAAAAACAACATGCAATTTCTATAA 900
DB 841 AAGATTTCTGTGTCATGAAAAATGTGTACTTAATAAAAAAACAACATGCAATTTCTATAA 900

QY 901 AGACGAATTTCTTTTAAATAATAAATTTCTTATAACAAATAAAGATAAGTGTCTCTTTAAA 960
DB 901 AGACGAATTTCTTTTAAATAATAAATTTCTTATAACAAATAAAGATAAGTGTCTCTTTAAA 960
QY 961 AACATGCAAAAGAAATATATAGATTTTACCGTATCAGATTTTTCATACAATTTTATATTTT 1020
DB 961 AACATGCAAAAGAAATATATAGATTTTACCGTATCAGATTTTTCATACAATTTTATATTTT 1020
QY 1021 TGAGCTTGAAGATTAACATGACAACTGTATCGTGTCTCTCGTCTATTTACCCCTAGA 1080
DB 1021 TGAGCTTGAAGATTAACATGACAACTGTATCGTGTCTCTCGTCTATTTACCCCTAGA 1080
QY 1081 AGAAGTGAACACATGAACTTTTATGTTTGCATACGGGAGCTAGCTTCTTCCCTACTTG 1140
DB 1081 AGAAGTGAACACATGAACTTTTATGTTTGCATACGGGAGCTAGCTTCTTCCCTACTTG 1140
QY 1141 TCCAAATAGATGAAGACATTTATCCTCAGTTCAGTCTTTCGAAAGCGCAACATATCGACA 1200
DB 1141 TCCAAATAGATGAAGACATTTATCCTCAGTTCAGTCTTTCGAAAGCGCAACATATCGACA 1200
QY 1201 AAAAATCGTTTGTAGCTCTATCATCTGTCTTTTGAAGAAAAATATCAACATATCAATACA 1260
DB 1201 AAAAATCGTTTGTAGCTCTATCATCTGTCTTTTGAAGAAAAATATCAACATATCAATACA 1260
QY 1261 TATACACACTCCCAAAATATATAACCAATATATATTTGGTAAAGAAAAATCAATATCAAT 1320
DB 1261 TATACACACTCCCAAAATATATAACCAATATATATTTGGTAAAGAAAAATCAATATCAAT 1320
QY 1321 GATATTTGCTTTTGAACCAACTTAACTGTGAATTA CAAGCTAAGCAATATATCTATTAT 1380
DB 1321 GATATTTGCTTTTGAACCAACTTAACTGTGAATTA CAAGCTAAGCAATATATCTATTAT 1380
QY 1381 AFTCTTTCTTTGTGTCTCAACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1440
DB 1381 AFTCTTTCTTTGTGTCTCAACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1440
QY 1441 TGTCTATTAATTTGAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1500
DB 1441 TGTCTATTAATTTGAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1500
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DB 1501 CTTAGTCTGATACGAAAACTTTATATAATATATATATATATATATATATATATATATAT 1560
QY 1561 TATTTTCTGTGTAATAAACAATCTTCTGATTAAGAACTATATAGTTAGGATATGTTGATCT 1620
DB 1561 TATTTTCTGTGTAATAAACAATCTTCTGATTAAGAACTATATAGTTAGGATATGTTGATCT 1620
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DB 1621 TGTGTGTGACATAGTAGGTCCTTAAAAAGAGGTCTGATTAATAATTTTACGTTTGGAC 1680
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DB 1681 CACAAATCTTTCTTTTGAATAATCGCGGACTGGGACACCTTCTCAACAACTGTCCGCTTT 1740
QY 1741 ACTAATCTTACGTACCCCTCACAATCTGTAACCAATAAATCAATAATAATATAGAGAC 1800
DB 1741 ACTAATCTTACGTACCCCTCACAATCTGTAACCAATAAATCAATAATAATATAGAGAC 1800
QY 1801 TGTGTGATCATTAATCGAAATATTTTTCTAATAATTTTTCTAATAATTTTTCTAATAATTTTT 1860
DB 1801 TGTGTGATCATTAATCGAAATATTTTTCTAATAATTTTTCTAATAATTTTTCTAATAATTTTT 1860
QY 1861 GGTATAACAATCAAGAAATCAAGAAAGAAATTTAAAAAACAACCTTGTGCAATCATGATTGAT 1920
DB 1861 GGTATAACAATCAAGAAATCAAGAAAGAAATTTAAAAAACAACCTTGTGCAATCATGATTGAT 1920
QY 1921 TTTTGGCTTATATCTTTCTAATTTTTTATATCTTTGTGCTGCAAAATTAGCACCACAAATATA 1980
DB 1921 TTTTGGCTTATATCTTTCTAATTTTTTATATCTTTGTGCTGCAAAATTAGCACCACAAATATA 1980
QY 1981 TATTTCTTCTTCTCAACATCGAATTTCTTTATTTTGTGTTAAAGGCAATTTTTTTTCTTAACAGA 2040

Db 1981 ||||| 1981 TATTCCTCTCTTCAACATCGAAATCTTATTTTGTAAAGCAATTTTTTCTTAAACAGA 2040
Qy 2041 GGAATTTTACATCATCTTCTAGACTGAACTTTTCGGGATAAAAATCTCGCATGCAAGGT 2100
Db 2041 GGAATTTTACATCATCTTCTAGACTGAACTTTTCGGGATAAAAATCTCGCATGCAAGGT 2100
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Db 2101 AATTTATTTTTCATGACAAAAGCCCAATGCGGATAATTAATACTAATACTATGCAA 2160
Qy 2161 AACGAACTTTTACTTTGGGTCTATACCGAGGAAAACAAGGTACACTCGATTTGTGCAACTC 2220
Db 2161 AACGAACTTTTACTTTGGGTCTATACCGAGGAAAACAAGGTACACTCGATTTGTGCAACTC 2220
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Db 2221 CACCAAGACCAACCCCACTTACCAATTTACCTTTATTTTGTCTTATTTCACTCAAAATCT 2280
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Db 2401 ATCTTTTGTGGGCACTTGTAACTGATGCAAAAAAATAAAAAAATAAAAAAATA 2460
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Qy 2701 AGTAATTTGATCTATGTTATACGACATCTACTTAATTTTGAAGAAAAAATA 2760
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Qy 2761 AACTATCTATACATGCTCCAAATTTATTTCTTGTCTTATGTAATTTATGCTATATTAG 2820
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Qy 2881 ATCATCATAGCAATTTTCAGTGTTTCAACCTTTATCGAATTCGACAAAGATTGAAACAA 2940
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Db 3301 TCTCTTATCCATTCAGCTCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3360
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Qy 3721 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3780
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Qy 3781 TGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3840
Db 3781 TGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3840
Qy 3841 AGATTTTCTACCGCATGGAATTTATCTCTTCAAAAAATAAAGATTTTAAAGTTTACTATG 3900
Db 3841 AGATTTTCTACCGCATGGAATTTATCTCTTCAAAAAATAAAGATTTTAAAGTTTACTATG 3900
Qy 3901 ACTTTAAATCTGAGTTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3960
Db 3901 ACTTTAAATCTGAGTTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3960
Qy 3961 ATCTGCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4020
Db 3961 ATCTGCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4020
Qy 4021 TGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4080
Db 4021 TGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4080
Qy 4081 AATTTAGTCAAAATTTATGTTAATATGCGACAGGAAACCAACATCAGCTAGAAATGTTGTC 4140
Db 4081 AATTTAGTCAAAATTTATGTTAATATGCGACAGGAAACCAACATCAGCTAGAAATGTTGTC 4140
Qy 4141 AACTGACAGCAACCTTAAATTTACTTACGGCAGCTCTCATCACCACCGACTTCTCAGGT 4200
Db 4141 AACTGACAGCAACCTTAAATTTACTTACGGCAGCTCTCATCACCACCGACTTCTCAGGT 4200

QY	4201	TGCAGGTTCCAGTCAAGCTAGAGTGAAATCAATGGTGGAAAGTGGCTCGATCGGAAAGT	4260	QY	5281	ATCTTTAAAGATCTTTCAAAAGTGTGAGTATGTTTATTTGGTTGGCTTCTGTGTGATATTTA	5340
Db	4201	TGCAGGTTCCAGTCAAGCTAGAGTGAAATCAATGGTGGAAAGTGGCTCGATCGGAAAGT	4260	Db	5281	ATCTTTAAAGATCTTTCAAAAGTGTGAGTATGTTTATTTGGTTGGCTTCTGTGTGATATTTA	5340
QY	4261	CCCATTTGCTGAAGCAGCTCTAAATTTGCCCTAGATGTCATCAACCAATACCTAAGTTCTG	4320	QY	5341	TGTTTATTAAGAAATTTGGTCTTATATATGCTATATATAGAGGTGGGTGATATGAT	5400
Db	4261	CCCATTTGCTGAAGCAGCTCTAAATTTGCCCTAGATGTCATCAACCAATACCTAAGTTCTG	4320	Db	5341	TGTTTATTAAGAAATTTGGTCTTATATATGCTATATATAGAGGTGGGTGATATGAT	5400
QY	4321	TTACTTCAATAACTATAGCTTACCTCAACCTCGCCATTTCTTGCAAAAATGTCGTGCTA	4380	QY	5401	GAAATCAAGAGTTCATGTTGGAAATCTTTTGTGTGTTTCTTGAATATCATCGAATTCCT	5460
Db	4321	TTACTTCAATAACTATAGCTTACCTCAACCTCGCCATTTCTTGCAAAAATGTCGTGCTA	4380	Db	5401	GAAATCAAGAGTTCATGTTGGAAATCTTTTGTGTGTTTCTTGAATATCATCGAATTCCT	5460
QY	4381	TTGGACAGCTGGCGGTTCTTGAGGAATGTTCTGTTGGAGGAGCTTTTGGAGGAACAA	4440	QY	5461	CAATTTCTTGAGACCCCAATATGAGACATCTAGACATCTATAGAACATATATGTAATGTA	5520
Db	4381	TTGGACAGCTGGCGGTTCTTGAGGAATGTTCTGTTGGAGGAGCTTTTGGAGGAACAA	4440	Db	5461	CAATTTCTTGAGACCCCAATATGAGACATCTAGACATCTATAGAACATATATGTAATGTA	5520
QY	4441	GAGAGCAAAATCCAGATCGAAATCTACGGTCTGTGCTCGACTGATAATACTACTAGTAC	4500	QY	5521	TATTAACAGTACTTAAGTTCGAAATTTTATGACCAAGTAAATATATGCGGAATGTACA	5580
Db	4441	GAGAGCAAAATCCAGATCGAAATCTACGGTCTGTGCTCGACTGATAATACTACTAGTAC	4500	Db	5521	TATTAACAGTACTTAAGTTCGAAATTTTATGACCAAGTAAATATATGCGGAATGTACA	5580
QY	4501	TTTCATCAGTCTTCTCGGCCAAGTTACTCAAAACCTTAGCAAGTTTCATAGCTACGGTCA	4560	QY	5581	TGCTAAATATCGAGTTTAAACTATTTTTCCTCAATATAACAACCTATTTCTTTTCCTCAA	5640
Db	4501	TTTCATCAGTCTTCTCGGCCAAGTTACTCAAAACCTTAGCAAGTTTCATAGCTACGGTCA	4560	Db	5581	TGCTAAATATCGAGTTTAAACTATTTTTCCTCAATATAACAACCTATTTCTTTTCCTCAA	5640
QY	4561	AATCCGGAGTTTAAATTCMACTTGGCCATCTTGGCTCTCTCBAAGCCTTGGAGATTA	4620	QY	5641	CTTATATCTCTTATCTGATTTCTTTTCTTTTAAATTCCTTTTCTTTTCTTTTCCCAA	5700
Db	4561	AATCCGGAGTTTAAATTCMACTTGGCCATCTTGGCTCTCTCBAAGCCTTGGAGATTA	4620	Db	5641	CTTATATCTCTTATCTGATTTCTTTTCTTTTAAATTCCTTTTCTTTTCTTTTCCCAA	5700
QY	4621	CAATTCAGCAACACTGGATAGATTTTGGTGGAACTCAAAATAGCAATGATAGTGG	4680	QY	5701	GACCAAAAAAATAACAGAAACGAAAAAAGAGATTTTAAAAATTCATAACCCAC	5760
Db	4621	CAATTCAGCAACACTGGATAGATTTTGGTGGAACTCAAAATAGCAATGATAGTGG	4680	Db	5701	GACCAAAAAAATAACAGAAACGAAAAAAGAGATTTTAAAAATTCATAACCCAC	5760
QY	4681	TATGAGTCTAGTGTGGGATCTTGGATGCATGGAGATPACCTCCATCACAACAAGCTCA	4740	QY	5761	GAGAAATATGACCTTAAATTCAGACTAATCCCAAAATTTTCAGAAATTTATGTAATTTTG	5820
Db	4681	TATGAGTCTAGTGTGGGATCTTGGATGCATGGAGATPACCTCCATCACAACAAGCTCA	4740	Db	5761	GAGAAATATGACCTTAAATTCAGACTAATCCCAAAATTTTCAGAAATTTATGTAATTTTG	5820
QY	4741	GCAATTCCTTTCTTGATCAACACTACCGGATTTGGTGGAACTTCAAAACGCTTATATCC	4800	QY	5821	CGATTTAATATTTGTCTTCACAATCATAATGCGCAACTAACTAAATGAAAAAGACAATGGAA	5880
Db	4741	GCAATTCCTTTCTTGATCAACACTACCGGATTTGGTGGAACTTCAAAACGCTTATATCC	4800	Db	5821	CGATTTAATATTTGTCTTCACAATCATAATGCGCAACTAACTAAATGAAAAAGACAATGGAA	5880
QY	4801	ATTACTAGAGGTAGGGAGGTGTTAATCAAGTGAATCTCAACAGAGAGTAGTGATTA	4860	QY	5881	TGACTGAACCAATGCATAATCTCTCAAGTCTCAACCTATGAAGATCATGTAACCAATAG	5940
Db	4801	ATTACTAGAGGTAGGGAGGTGTTAATCAAGTGAATCTCAACAGAGAGTAGTGATTA	4860	Db	5881	TGACTGAACCAATGCATAATCTCTCAAGTCTCAACCTATGAAGATCATGTAACCAATAG	5940
QY	4861	TTCCCAATCAGCTAAATGTTTAAAGCCCTTGATGGATTTTCTTCAAGGCGGTTAGCGCCAC	4920	QY	5941	ACTATCATCATGATTTAGTTAATGCAATGATCTATATGATTTCTTTGAAACATAGATGTC	6000
Db	4861	TTCCCAATCAGCTAAATGTTTAAAGCCCTTGATGGATTTTCTTCAAGGCGGTTAGCGCCAC	4920	Db	5941	ACTATCATCATGATTTAGTTAATGCAATGATCTATATGATTTCTTTGAAACATAGATGTC	6000
QY	4921	GCAACAAGAAATGTGAAGCGGAGAGAAATGATCAGGATCGGGTAGGGATGGGATGG	4980	QY	6001	ATTTATCTGGATATAAAGATGGCGTTTAAACCTACTTTTGCAATTTTGTATATCTTTCT	6060
Db	4921	GCAACAAGAAATGTGAAGCGGAGAGAAATGATCAGGATCGGGTAGGGATGGGATGG	4980	Db	6001	ATTTATCTGGATATAAAGATGGCGTTTAAACCTACTTTTGCAATTTTGTATATCTTTCT	6060
QY	4981	AGTGAATACTTATCAAGAACTTTTGGGTAATATCAACATATACTCAGGAGGAAACGA	5040	QY	6061	TCATAATACATATGATCAATACACTTTTGTTTTAAAAAGAAATTAATACTTTATTTCAAC	6120
Db	4981	AGTGAATACTTATCAAGAACTTTTGGGTAATATCAACATATACTCAGGAGGAAACGA	5040	Db	6061	TCATAATACATATGATCAATACACTTTTGTTTTAAAAAGAAATTAATACTTTATTTCAAC	6120
QY	5041	GGAATACATCATGCGGAGGTAAACAGTTCTTGGACCGGTTTCACTCCAACTCAAC	5100	QY	6121	ATCGATCAATTTTACCTTTTGTTCCTATATGACTACATTTTATAGGCTCACACTTTGT	6180
Db	5041	GGAATACATCATGCGGAGGTAAACAGTTCTTGGACCGGTTTCACTCCAACTCAAC	5100	Db	6121	ATCGATCAATTTTACCTTTTGTTCCTATATGACTACATTTTATAGGCTCACACTTTGT	6180
QY	5101	AGGCCATCTCTCAATCTAAGTACTCAGCACTAGCTATTTCTTGATGATTTCTTTTGGTT	5160	QY	6181	TTCCGATCTAGATATACATCAATCCACTTTGTTGAGACGTTGGTGGAAAGTCTTCTT	6240
Db	5101	AGGCCATCTCTCAATCTAAGTACTCAGCACTAGCTATTTCTTGATGATTTCTTTTGGTT	5160	Db	6181	TTCCGATCTAGATATACATCAATCCACTTTGTTGAGACGTTGGTGGAAAGTCTTCTT	6240
QY	5161	GGGGTGTACATTTGGTCTGTATGCGAGTTATGCTGAGGAGATCAAAACCATGCGCT	5220	QY	6241	TTTTCACAGATGTTTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGTAGGCAAT	6300
Db	5161	GGGGTGTACATTTGGTCTGTATGCGAGTTATGCTGAGGAGATCAAAACCATGCGCT	5220	Db	6241	TTTTCACAGATGTTTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGTAGGCAAT	6300
QY	5221	ATATCCAAAGGCTAAATTTGAGGCTCAAGGAAAGGTATGGTTATATAAACTATCTTTTG	5280	QY	6301	CTTGAAACGATAGCCTTTCTTTATCGCAATGATGCAATTTGTAGAGCCATCTTCTTTT	6360
Db	5221	ATATCCAAAGGCTAAATTTGAGGCTCAAGGAAAGGTATGGTTATATAAACTATCTTTTG	5280	Db	6301	CTTGAAACGATAGCCTTTCTTTATCGCAATGATGCAATTTGTAGAGCCATCTTCTTTT	6360
				QY	6361	CTACTGTCTTTTCGATGAAGTGACAGATAGTCTGGGCAATGGAATCCGAGGAGTTTCCCG	6420

Db 6361 |||||CTACTGTCCTTTTCGATGAAGTACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCG 6420
Qy 6421 ATATTACCCCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGA 6480
Db 6421 ATATTACCCCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGA 6480
Qy 6481 TATTCTTGAGTAGACGAGAGTGTGCTGTCCACCATGTTGGGATCTAGATATCAATC 6540
Db 6481 TATTCTTGAGTAGACGAGAGTGTGCTGTCCACCATGTTGGGATCTAGATATCAATC 6540
Qy 6541 AATCCACTTGTCTTGAAGACGTGTTGGAACGTCTTCTTTTCCACGATGTTCTCGTG 6600
Db 6541 AATCCACTTGTCTTGAAGACGTGTTGGAACGTCTTCTTTTCCACGATGTTCTCGTG 6600
Qy 6601 GTGGGGTCCATCTTTTGGGACCACTGTGCGTAGAGGCATCTTGAACGATAGCCTTTCC 6660
Db 6601 GTGGGGTCCATCTTTTGGGACCACTGTGCGTAGAGGCATCTTGAACGATAGCCTTTCC 6660
Qy 6661 TATCGCAATGATGGCAATTTGTAGAAGCAATCTTCTTCTACTGTCTTTCGATGAAGT 6720
Db 6661 TATCGCAATGATGGCAATTTGTAGAAGCAATCTTCTTCTACTGTCTTTCGATGAAGT 6720
Qy 6721 GACAGATAGCTGGGCAATGGAATCCGAGGAGTTCGCGATATACCCCTTGTGAAAG 6780
Db 6721 GACAGATAGCTGGGCAATGGAATCCGAGGAGTTCGCGATATACCCCTTGTGAAAG 6780
Qy 6781 TCTCAATAGCCCTCTGCTCTTGAGACTGTATCTTTTGATATCTTGGAGTAGACGAG 6840
Db 6781 TCTCAATAGCCCTCTGCTCTTGAGACTGTATCTTTTGATATCTTGGAGTAGACGAG 6840
Qy 6841 TCTCGTGTCCACCAATGTTGGGATCTAGATATCAATCAATCCACTTGTGAAAG 6900
Db 6841 TCTCGTGTCCACCAATGTTGGGATCTAGATATCAATCAATCCACTTGTGAAAG 6900
Qy 6901 TGGTTGGACGCTCTTCTTTTCCAGATGTTCTGCTGGTGGGGTCCATCTTTGGGAC 6960
Db 6901 TGGTTGGACGCTCTTCTTTTCCAGATGTTCTGCTGGTGGGGTCCATCTTTGGGAC 6960
Qy 6961 CACTGTGCGTAGAGGCATCTTGAACGATAGCCCTTCTTTATCGCAATGATGGCATTTGT 7020
Db 6961 CACTGTGCGTAGAGGCATCTTGAACGATAGCCCTTCTTTATCGCAATGATGGCATTTGT 7020
Qy 7021 AGAAGCCATCTTCTTTCTACTGTCTTTCGATGAAGTGACAGATAGCTGGGCAATGGA 7080
Db 7021 AGAAGCCATCTTCTTTCTACTGTCTTTCGATGAAGTGACAGATAGCTGGGCAATGGA 7080
Qy 7081 ATCCGAGAGGTTTCCGATATATACCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTT 7140
Db 7081 ATCCGAGAGGTTTCCGATATATACCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTT 7140
Qy 7141 CTGAGACTGTATCTTTGATATTTCTGGAGTAGACGAGAGTGTGCTGCCACCATGTTGG 7200
Db 7141 CTGAGACTGTATCTTTGATATTTCTGGAGTAGACGAGAGTGTGCTGCCACCATGTTGG 7200
Qy 7201 GGACTCTAGATATACATCAATCCACTTGTCTTGAAGACGTGTTGGAACGTCTTCTTTT 7260
Db 7201 GGACTCTAGATATACATCAATCCACTTGTCTTGAAGACGTGTTGGAACGTCTTCTTTT 7260
Qy 7261 CCACAGATGTTCTGCTGGTGGGGTCCATCTTTTGGGACCATGTGCGTAGAGGCATCTT 7320
Db 7261 CCACAGATGTTCTGCTGGTGGGGTCCATCTTTTGGGACCATGTGCGTAGAGGCATCTT 7320
Qy 7321 GAAACGATAGCCTTCTTCTTATCGCAATGATGTCATTTGTAGAAGCCATCTTCTTTTCTA 7380
Db 7321 GAAACGATAGCCTTCTTCTTATCGCAATGATGTCATTTGTAGAAGCCATCTTCTTTTCTA 7380
Qy 7381 CTGTCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATA 7440
Db 7381 CTGTCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATA 7440
Qy 7441 TTACCCCTTTGTTGAAAGTCTCAATAGCCCTCTGCTCTTGAGACTGTATCTTTGATAT 7500

Db 7441 TTACCCCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATAT 7500
Qy 7501 TCTTGGAGTAGACGAGAGTGTGCTGTCCACCATGTTGGGATCCACTAGTTCTAGAGCG 7560
Db 7501 TCTTGGAGTAGACGAGAGTGTGCTGTCCACCATGTTGGGATCCACTAGTTCTAGAGCG 7560
Qy 7561 GCCGCCACCGCGTGGAGCT 7580
Db 7561 GCCGCCACCGCGTGGAGCT 7580
RESULT 2
ADL71846
ID ADL71846 standard; DNA; 1746 BP.
XX
AC ADL71846;
XX
DT 20-MAY-2004 (first entry)
XX
DE Arabidopsis thaliana OBP3 antisense DNA #7.
XX
KW Transgenic plant; Dof transcription factor; ocs binding factor;
KW plant size; plant stature; root growth; plant; gene; ds; OBF;
KW OBF binding protein; OBP3; SOB1; mouse-ear cress.
XX
OS Arabidopsis thaliana.
XX
PN US2004045055-A1.
XX
PD 04-MAR-2004.
XX
PF 28-AUG-2003; 2003US-00650249.
XX
PR 28-AUG-2002; 2002US-0406657P.
XX:
PA (UNIW) UNIV WASHINGTON.
XX
PI Neff MM;
XX
XX WPI; 2004-225757/21.
PT New transgenic plant cell, useful in producing plants with altered size
PT and stature and with normal and healthy root growth.
PS Claim 38; SEQ ID NO 18; 53pp; English.
XX
CC The invention relates to a transgenic plant transformed by a Dof
CC transcription factor, OBF (ocs binding factor) binding protein (OBP3).
CC OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic
CC acid and polypeptides are useful in producing transgenic plants with
CC altered size and stature and with normal and healthy root growth. The
CC present sequence is Arabidopsis thaliana OBP3 antisense DNA.
XX
SQ Sequence 1746 BP; 560 A; 304 C; 304 G; 578 T; 0 U; 0 Other;
Query Match 22.8%; Score 1730; DB 12; Length 1746;
Best Local Similarity 99.8%; Pred. No. 2.6e-258;
Matches 1743; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
Qy 4436 AACAGAGAAGCAATCCAGATCGAAATCTAGCGTGGTCTCGACTGATAATACTACT 4495
Db 1 AACAGAGAAGCAATCCAGATCGAAATCTAGCGTGGTCTCGACTGATAATACTACT 60
Qy 4496 AGTACTTTCATCTTACTTCTCGCCCAAGTTACTCAAAACCCCTAGCAAGTTTCATAGCTAC 4555
Db 61 AGTACTTTCATCTTACTTCTCGCCCAAGTTACTCAAAACCCCTAGCAAGTTTCATAGCTAC 120
Qy 4556 GGTCAAAATCCCGAGTTTAAATTCACATTTGCCCATCTTTGCCCTCTCCAAAGCCTTGA 4615
Db 121 GGTCAAAATCCCGAGTTTAAATTCACATTTGCCCATCTTTGCCCTCTCCAAAGCCTTGA 180
Qy 4616 GATTACAATTCAGCAACACTGGATTAGATTTTGTGGAACTCAAAATAGCAATGATA 4675

Db 181 GATTACAATTCAAGCAACACTGGATTAGATTGTTGGTGAACCTCAAAATGAAGCAACATGATA 240
Qy 4676 AGTGGTATGAGTTCTAGTGGTGGGATCTTGATGCATGGAGATACCTCCATCAACAA 4735
Db 241 AGTGGTATGAGTTCTAGTGGTGGGATCTTGATGCATGGAGATACCTCCATCAACAA 300
Qy 4736 GCTCAGCAATCCCTTTCTTGATCAACACTACCGGATTTGGTGCATCTTCAACCGCGTTA 4795
Db 301 GCTCAGCAATCCCTTTCTTGATCAACACTACCGGATTTGGTGCATCTTCAACCGCGTTA 360
Qy 4796 TATCCATTACTAGAAAGTGAAGGGAGTGTAAATCAAGGTGATTTCTCAACAGAAGAGTAGT 4855
Db 361 TATCCATTACTAGAAAGTGAAGGGAGTGTAAATCAAGGTGATTTCTCAACAGAAGAGTAGT 420
Qy 4856 GATTATTCGAATCAGCTAATGTTTAAAGCCCTTGATGGATTTTCTTCAAGCGGGTTAGC 4915
Db 421 GATTATTCGAATCAGCTAATGTTTAAAGCCCTTGATGGATTTTCTTCAAGCGGGTTAGC 480
Qy 4916 GCCAGCAACCAAGAAATGTGAAGCGGAAGAGATGATCAGGATCGGGGTAGGATGGG 4975
Db 481 GCCAGCAACCAAGAAATGTGAAGCGGAAGAGATGATCAGGATCGGGGTAGGATGGG 540
Qy 4976 GATGAGTGAATAACTTATCAAGAACTTTTGGGTAATATCAACATAAACTCAGGCAGG 5035
Db 541 GATGAGTGAATAACTTATCAAGAACTTTTGGGTAATATCAACATAAACTCAGGCAGG 600
Qy 5036 AACGAGGAATACACATCATATGAGGAGGTAAACAGTCTTGGAACGGTTTCACTCCAAACAC 5095
Db 601 AACGAGGAATACACATCATATGAGGAGGTAAACAGTCTTGGAACGGTTTCACTCCAAACAC 660
Qy 5096 TCAACAGGCCATCTCTCATTC--TAAGTACTCAGCACTAGCTATTTCTTGATGATCTTT 5152
Db 661 TCAACAGGCCATCTCTCATTC--TAAGTACTCAGCACTAGCTATTTCTTGATGATCTTT 720
Qy 5153 TGTGTTGGGTGTACATGCTGCTGTGTCGCGAGTTATTGCTGAGGAAGATCAAAACC 5212
Db 721 TGTGTTGGGTGTACATGCTGCTGTGTCGCGAGTTATTGCTGAGGAAGATCAAAACC 780
Qy 5213 ATGCACTATATCCAAAGGCTAATTTGAGGCTCAAGAAAGGTATGGTTTAAACCTA 5272
Db 781 ATGCACTATATCCAAAGGCTAATTTGAGGCTCAAGAAAGGTATGGTTTAAACCTA 840
Qy 5273 TCTTTTGTATCTTTTAAAGATCTTCAAGTGTGAGTATGTTTATTTGTTGGCTTCTGCT 5332
Db 841 TCTTTTGTATCTTTTAAAGATCTTCAAGTGTGAGTATGTTTATTTGTTGGCTTCTGCT 900
Qy 5333 GATATTTATGTTTATTAGAAATTTGCTCTATATATTGGCTATATATAGAGGTGTGGGTG 5392
Db 901 GATATTTATGTTTATTAGAAATTTGCTCTATATATTGGCTATATATAGAGGTGTGGGTG 960
Qy 5393 ATATGTATGAATTCAGAGTGTGATGTGGAACCTTTTGTGTGTTTCATTTGAATATCAT 5452
Db 961 ATATGTATGAATTCAGAGTGTGATGTGGAACCTTTTGTGTGTTTCATTTGAATATCAT 1020
Qy 5453 CGAATTTCAATTTCTTGAGACCCATTTATGACATTCAGACATCTATAGACATATAT 5512
Db 1021 CGAATTTCAATTTCTTGAGACCCATTTATGACATTCAGACATCTATAGACATATAT 1080
Qy 5513 GTAACTGATATTAACGTTACTTAAAGTCGAATTTTATGACCAAGTAAATATATGCGG 5572
Db 1081 GTAACTGATATTAACGTTACTTAAAGTCGAATTTTATGACCAAGTAAATATATGCGG 1140
Qy 5573 AATGTACATGCTAATATCAGTGTAAACCTATTTTCCAAATATAACAACTATTTTCTCTT 5632
Db 1141 AATGTACATGCTAATATCAGTGTAAACCTATTTTCCAAATATAACAACTATTTTCTCTT 1200
Qy 5633 TGTGCAACTATATATCTTATCTGATCTTATTTTCTTCTTTTAAATCTCTTTTCC 5692
Db 1201 TGTGCAACTATATATCTTATCTGATCTTATTTTCTTCTTTTAAATCTCTTTTCC 1260
Qy 5693 TTTTCCCAAGACACAAAAAATAACAGAAACGAAAAAGAGATTTTAAAAATTTCA 5752
Db 1261 TTTTCCCAAGACACAAAAAATAACAGAAACGAAAAAGAGATTTTAAAAATTTCA 1320

Qy 5753 TAACCCAGGAAATTATGCACCTAAATTCAGACTAAATCCCCCAAAATTCAGAAATTTATG 5812
Db 1321 TAACCCAGGAAATTATGCACCTAAATTCAGACTAAATCCCCCAAAATTCAGAAATTTATG 1380
Qy 5813 TATTTTGGGATTTAAATTAATTTGTGTTCAATCATATAATGGCCAACTTAACATAATGAAAGA 5872
Db 1381 TATTTTGGGATTTAAATTAATTTGTGTTCAATCATATAATGGCCAACTTAACATAATGAAAGA 1440
Qy 5873 CAATGGATGACTCAAAACCATGATTAATCTCAAGTCTCAACCTATGAAGAATCATGTA 5932
Db 1441 CAATGGATGACTCAAAACCATGATTAATCTCAAGTCTCAACCTATGAAGAATCATGTA 1500
Qy 5933 ACCAATGACTATCATCATGATTAATTAATGATGATCTATAATGTTATTTTGAACATA 5992
Db 1501 ACCAATGACTATCATCATGATTAATTAATGATGATCTATAATGTTATTTTGAACATA 1560
Qy 5993 GATATGCTAATTTCTCGATATAAAGATGGCGTTTAACTTACCTTGGCAATTTTGTAT 6052
Db 1561 GATATGCTAATTTCTCGATATAAAGATGGCGTTTAACTTACCTTGGCAATTTTGTAT 1620
Qy 6053 ATCTTTCTTCTAAATACATGATCAATACACTTTTGTGTTTAAAGAAATTTAAAACTTA 6112
Db 1621 ATCTTTCTTCTAAATACATGATCAATACACTTTTGTGTTTAAAGAAATTTAAAACTTA 1680
Qy 6113 TTTCAACATCGATCAACATTTTACTTTTGTGTTTCCATATTTGACTACATTTATAGCTCAC 6172
Db 1681 TTTCAACATCGATCAACATTTTACTTTTGTGTTTCCATATTTGACTACATTTATAGCTCAC 1740
Qy 6173 ACTTTT 6178
Db 1741 ACTTTT 1746

RESULT 3

ABQ73047/c

ID ABQ73047 standard; DNA; 10078 BP.

XX ABQ73047;

XX 24-SEP-2002 (first entry)

XX Tomato anthocyanin 1 (ANT1) related plasmid pAG3202 SEQ ID NO:3.

XX Tomato; ANT1; anthocyanin 1; Lycopersicon esculentum; plant; colour;
gene; ds.

XX Lycopersicon esculentum.
OS Synthetic.

XX WO200255658-A2.

XX 18-JUL-2002.

XX 29-OCT-2001; 2001WO-US050638.

XX 30-OCT-2000; 2000US-0244685P.

XX (EXEL-) EXELIXIS PLANT SCI INC.

XX Connors K, Mathews HV, Liu A;

XX WPI; 2002-557819/59.

XX New isolated polynucleotide derived from tomato, useful for producing an
PT Anthocyanin 1 phenotype in plants, particularly for modifying e.g. leaf
PT color, flower color or fruit color in plants.

XX Example 1; Page 41-46; 53pp; English.

XX The present invention describes tomato anthocyanin 1 (ANT1). The ANT1
CC polynucleotide can be used for modifying the expression of a native plant
CC gene, particularly for producing an anthocyanin 1 phenotype in plants,

CC which is responsible for many red and blue colours in plants. The
CC polynucleotide is useful for modifying e.g. leaf colour, flower colour or
CC fruit colour in plants. The present sequence represents the plasmid
CC pAG3202 which is used in an example from the present invention for the
CC generation of plants with an AN1 phenotype by transformation with an
CC activation tagging construct

XX
SQ Sequence 10078 BP; 2533 A; 2568 C; 2625 G; 2333 T; 0 U; 19 Other;

Query Match 18.5%; Score 1402.4; DB 6; Length 10078;
Best Local Similarity 99.9%; Pred. No. 1.3e-207;
Matches 1403; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	6177	TTGTTTCGATCTAGATATCATCAATCCATCTGCTTTGAAGACGTGGTTGGAACGCT	6236
Db	4251	TAGTTTCGATCTAGATATCATCAATCCATCTGCTTTGAAGACGTGGTTGGAACGCT	4192
QY	6237	TCCTTTTCCACCATGTTCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAG	6296
Db	4191	TCCTTTTCCACCATGTTCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAG	4132
QY	6297	GCATCTTGAAAGATAGCTTTCCCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCC	6356
Db	4131	GCATCTTGAAAGATAGCTTTCCCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCC	4072
QY	6357	TTTTCTACTGCTTTTCGATGAAGTGA CAGATAGCTGGGCAATGGAATCCGAGAGGTTT	6416
Db	4071	TTTTCTACTGCTTTTCGATGAAGTGA CAGATAGCTGGGCAATGGAATCCGAGAGGTTT	4012
QY	6417	CCCGATATTACCTTTGTTGAAAGTCTCAATAGCCCTCTGCTCTCTGAGACTGATCT	6476
Db	4011	CCCGATATTACCTTTGTTGAAAGTCTCAATAGCCCTCTGCTCTCTGAGACTGATCT	3952
QY	6477	TTGATATTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCAATGTTGGGATCTAGATATCA	6536
Db	3951	TTGATATTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCAATGTTGGGATCTAGATATCA	3892
QY	6537	CATCAATCCATGCTTTTGAAGACGTGGTGAACGCTCTCTTTTCCACGATGTTCTCTC	6596
Db	3891	CATCAATCCATGCTTTTGAAGACGTGGTGAACGCTCTCTTTTCCACGATGTTCTCTC	3832
QY	6597	GTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGGGCATCTTGAACGATAGCCCTT	6656
Db	3831	GTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGGGCATCTTGAACGATAGCCCTT	3772
QY	6657	CTTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTTCTACTGCTCTTTCGATG	6716
Db	3771	CTTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTTCTACTGCTCTTTCGATG	3712
QY	6717	AAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCCCTTTTGA	6776
Db	3711	AAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCCCTTTTGA	3652
QY	6777	AAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGATCTTTGATATTCTTGGAGTAGACG	6836
Db	3651	AAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGATCTTTGATATTCTTGGAGTAGACG	3592
QY	6837	AGAGTGTGCTGCTCCACCATGTTGGGATCTAGATATCATCAATCCATCTGCTTGA	6896
Db	3591	AGAGTGTGCTGCTCCACCATGTTGGGATCTAGATATCATCAATCCATCTGCTTGA	3532
QY	6897	GACGTGGTTGGAACGCTTTCTTTTCCACGATGTTCTCGTGGTGGGGTCCATCTTTG	6956
Db	3531	GACGTGGTTGGAACGCTTTCTTTTCCACGATGTTCTCGTGGTGGGGTCCATCTTTG	3472
QY	6957	GAACCATGTCGGTAGAGCATCTTGAACGATAGCTTTCTTTATCGCAATGATGGCAT	7016
Db	3471	GAACCATGTCGGTAGAGCATCTTGAACGATAGCTTTCTTTATCGCAATGATGGCAT	3412
QY	7017	TTGTAGAGCCATCTTCTCTTCTACTGTCCTTTTCGATGAAGTGA CAGATAGCTGGCAA	7076
Db	3411	TTGTAGAGCCATCTTCTCTTCTACTGTCCTTTTCGATGAAGTGA CAGATAGCTGGCAA	3352

QY	7077	TGGAATCCGAGAGCTTTCCCGATATTACCTTTGTTGAAAGTCTCAATAGCCCTCTGG	7136
Db	3351	TGGAATCCGAGAGCTTTCCCGATATTACCTTTGTTGAAAGTCTCAATAGCCCTCTGG	3292
QY	7137	TCCTCTGAGACTGTATCTTTGATATTTTGGAGTAGACGAGAGTGTGCTGCCACCATG	7196
Db	3291	TCCTCTGAGACTGTATCTTTGATATTTTGGAGTAGACGAGAGTGTGCTGCCACCATG	3232
QY	7197	TTGGGATCTAGATATCATCAATCCATCTTCTTTGAAGACGTGGTTGGAACGCTTCT	7256
Db	3231	TTGGGATCTAGATATCATCAATCCATCTTCTTTGAAGACGTGGTTGGAACGCTTCT	3172
QY	7257	TTTTTCCAGATGTTCTCTGTTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCA	7316
Db	3171	TTTTTCCAGATGTTCTCTGTTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCA	3112
QY	7317	TCCTTGAACGATAGCCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTT	7376
Db	3111	TCCTTGAACGATAGCCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTT	3052
QY	7377	TCTACTGCTCTTTTCGATGAAGTGA CAGATAGCTGGGCAATGGAATCCGAGAGGTTTCC	7436
Db	3051	TCTACTGCTCTTTTCGATGAAGTGA CAGATAGCTGGGCAATGGAATCCGAGAGGTTTCC	2992
QY	7437	GATATTACCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG	7496
Db	2991	GATATTACCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG	2932
QY	7497	ATATTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTTGGGATCCACTAGTCTAG	7556
Db	2931	ATATTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTTGGGATCCACTAGTCTAG	2872
QY	7557	AGCGGCCCCACCGCGGTGGAGCT 7580	
Db	2871	AGCGGCCCCACCGCGGTGGAGCT 2848	

RESULT 4

ADV39061/c
ID ADV39061 standard; DNA; 17511 BP.
XX
AC ADV39061;
XX
DT 24-FEB-2005 (first entry)
XX
DE Plant gene activation vector-related DNA sequence pHR-AT - SEQ ID 13.
XX
KW gene activation vector; genetic analysis; ds.
XX
OS Unidentified.
XX
PN WO2004106520-A1.
XX
PD 09-DEC-2004.
XX
PF 28-MAY-2004; 2004WO-JP007789.
XX
PR 30-MAY-2003; 2003JP-00153985.
XX
PA (RIKE) RIKEN KK.
XX
PI Muranaka T, Seki H;
XX
DR WPI; 2005-021291/02.
XX
PT Novel plant gene active vector comprising hairy-root induction gene, and
PT enhancer and/or promoter that functions in plant, useful for activating
PT plant gene forming hairy root.
XX
PS Claim 4; SEQ ID NO 13; 54pp; Japanese.
XX
XX The invention comprises a plant gene activation vector that contains a
CC hairy-root induction gene and enhancer and/or promoter which can function

CC in a plant. The vector of the invention is useful for analyzing a plant
CC gene. The present DNA sequence is claimed in the invention.

XX SQ Sequence 17511 BP; 4453 A; 4201 C; 4511 G; 4344 T; 0 U; 2 Other;
Query Match 18.0%; Score 1367.4; DB 14; Length 17511;
Best Local Similarity 99.9%; Pred. No. 3.4e-202;
Matches 1368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6177 TTGTTTCGGATCTAGATATCATCAATCCATCTCTTTTGAAGACGTTGGAAAGCTCT 6236
DB 17505 TAGTTTCGGATCTAGATATCATCAATCCATCTCTTTTGAAGACGTTGGAAAGCTCT 17446
QY 6237 TCTTTTTCACGATGTTCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAG 6296
DB 17445 TCTTTTTCACGATGTTCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAG 17386
QY 6297 GCATCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCATTTCTGAAGCCATCTTCC 6356
DB 17385 GCATCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCATTTCTGAAGCCATCTTCC 17326
QY 6357 TTTTCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTT 6416
DB 17325 TTTTCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTT 17266
QY 6417 CCCGATATTAACCTTTTGTGAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCT 6476
DB 17265 CCCGATATTAACCTTTTGTGAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCT 17206
QY 6477 TTGATATCTTCGAGTGACGAGAGTGCTGCTCCACCATGTTGGGATCTAGATATCA 6536
DB 17205 TTGATATCTTCGAGTGACGAGAGTGCTGCTCCACCATGTTGGGATCTAGATATCA 17146
QY 6537 CATCAATCCACTTGCTTTGAAGACGTTGTTGAACGTCCTTCTTTTCCACGATGTTCCCT 6596
DB 17145 CATCAATCCACTTGCTTTGAAGACGTTGTTGAACGTCCTTCTTTTCCACGATGTTCCCT 17086
QY 6597 GTGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGGGCATCTTGAACGATAGCCTTT 6656
DB 17085 GTGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGGGCATCTTGAACGATAGCCTTT 17026
QY 6657 CTTTATCCGATGATGGCATTTGTAGAGCCATCTTCTTTTCTACTGTCCTTTCGATG 6716
DB 17025 CTTTATCCGATGATGGCATTTGTAGAGCCATCTTCTTTTCTACTGTCCTTTCGATG 16966
QY 6717 AAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTAACCTTTGTTGA 6776
DB 16965 AAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTAACCTTTGTTGA 16906
QY 6777 AAGTCTCAATAGCCTCTGCTCTTCTGAGACTGTATCTTTGATATCTTGGAGTAGAGC 6836
DB 16905 AAGTCTCAATAGCCTCTGCTCTTCTGAGACTGTATCTTTGATATCTTGGAGTAGAGC 16846
QY 6837 AGAGTGTCTGTCTCCACCATGTTGGGATCTAGATATCAATCAATCCACTTGTCTTGA 6896
DB 16845 AGAGTGTCTGTCTCCACCATGTTGGGATCTAGATATCAATCAATCCACTTGTCTTGA 16786
QY 6897 GAGTGTGTTGGAACGTCCTTTTCCAGATGTTCTCGTGGTGGGGTCCATCTTTG 6956
DB 16785 GAGTGTGTTGGAACGTCCTTTTCCAGATGTTCTCGTGGTGGGGTCCATCTTTG 16726
QY 6957 GGAACCACTGTCGGTAGAGCATCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCAT 7016
DB 16725 GGAACCACTGTCGGTAGAGCATCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCAT 16666
QY 7017 TTGTAGAAGCCATCTTCTTTTCTACTGTCCTTTCCATGATGAGTACAGATAGCTGGCAA 7076
DB 16665 TTGTAGAAGCCATCTTCTTTTCTACTGTCCTTTCCATGATGAGTACAGATAGCTGGCAA 16606
QY 7077 TGGAAATCCGAGGAGTTTCCCGATATTAACCTTTGTTGAAAGTCTCAATAGCCCTCTCG 7136
DB 16605 TGGAAATCCGAGGAGTTTCCCGATATTAACCTTTGTTGAAAGTCTCAATAGCCCTCTCG 16546

QY 7137 TCTTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAGAGTGTCTGCTCCACCATG 7196
DB 16545 TCTTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAGAGTGTCTGCTCCACCATG 16486
QY 7197 TTGGGGATCTAGATATCACATCAATCCACTTTCGTTTGAAGACGTTGGAAAGCTCTTCT 7256
DB 16485 TTGGGGATCTAGATATCACATCAATCCACTTTCGTTTGAAGACGTTGGAAAGCTCTTCT 16426
QY 7257 TTTTCCACGATGTTCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCA 7316
DB 16425 TTTTCCACGATGTTCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCA 16366
QY 7317 TCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTT 7376
DB 16365 TCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTT 16306
QY 7377 TCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCC 7436
DB 16305 TCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCC 16246
QY 7437 GATATTACCTTTTGTGAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTG 7496
DB 16245 GATATTACCTTTTGTGAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTG 16186
QY 7497 ATATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCC 7545
DB 16185 ATATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCC 16137

RESULT 5

ADV39062/c

ID ADV39062 standard; DNA; 18987 BP.

XX AC ADV39062;

XX DT 24-FEB-2005 (first entry)

XX DE Plant gene activation vector-related DNA sequence pHR-AT-GFP - SEQ ID 14.

XX KW gene activation vector; genetic analysis; ds.

XX OS Unidentified.

XX PN WO2004106520-A1.

XX PD 09-DEC-2004.

XX PF 28-MAY-2004; 2004WO-JP007789.

XX PR 30-MAY-2003; 2003JP-00153985.

XX PA (RIKE) RIKEN KK.

XX PI Muranaka T, Seki H;

XX DR WPI; 2005-021291/02.

XX PT Novel plant gene active vector comprising hairy-root induction gene, and
enhancer and/or promoter that functions in plant, useful for activating
plant gene forming hairy root.

XX PS Claim 5; SEQ ID NO 14; 54pp; Japanese.

XX CC The invention comprises a plant gene activation vector that contains a
hairy-root induction gene and enhancer and/or promoter which can function
in a plant. The vector of the invention is useful for analyzing a plant
gene. The present DNA sequence is claimed in the invention.

XX SQ Sequence 18987 BP; 4871 A; 4609 C; 4863 G; 4642 T; 0 U; 2 Other;

Query Match 18.0%; Score 1367.4; DB 14; Length 18987;
Best Local Similarity 99.9%; Pred. No. 3.4e-202;
Matches 1368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	6177	TTGTTTCGATCTAGATATCAATCAATCAATCAATCTTGTCTTTGAAGACGTGTTGGAACGTCT	6236
Db	18981	TAGTTTCGATCTAGATATCAATCAATCAATCAATCTTGTCTTTGAAGACGTGTTGGAACGTCT	18922
QY	6237	TCCTTTTCCACGATGTTCTCGTGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAG	6296
Db	18921	TCCTTTTCCACGATGTTCTCGTGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAG	18862
QY	6297	GCATCTTGAACGATAGCTTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCC	6356
Db	18861	GCATCTTGAACGATAGCTTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCC	18802
QY	6357	TTTTTCTACTGCTTTTCGATGAAGTGACAGATAGCTGGGCAATCGAATCCGAGAGGTTT	6416
Db	18801	TTTTTCTACTGCTTTTCGATGAAGTGACAGATAGCTGGGCAATCGAATCCGAGAGGTTT	18742
QY	6417	CCCGATATTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCT	6476
Db	18741	CCCGATATTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCT	18682
QY	6477	TTGATATTCTTGGAGTAGACGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCA	6536
Db	18681	TTGATATTCTTGGAGTAGACGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCA	18622
QY	6537	CATCAATCCACTTGTCTTGAAGACGTTGGAACGTCCTTTTTCACGATGTTCTTC	6596
Db	18621	CATCAATCCACTTGTCTTGAAGACGTTGGAACGTCCTTTTTCACGATGTTCTTC	18562
QY	6597	GTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTT	6656
Db	18561	GTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTT	18502
QY	6657	CTTTATCCCAATGATGGCAATTTGTAAGACCATCTTCTTCTACTGCTCTTTCGATG	6716
Db	18501	CTTTATCCCAATGATGGCAATTTGTAAGACCATCTTCTTCTACTGCTCTTTCGATG	18442
QY	6717	AAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCGATATTAACCTTTGTGA	6776
Db	18441	AAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCGATATTAACCTTTGTGA	18382
QY	6777	AAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGAG	6836
Db	18381	AAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGAG	18322
QY	6837	AGAGTGTCTGCTCCACCATGTTGGGATCTAGATATCAATCAATCAATCTTCTTGA	6896
Db	18321	AGAGTGTCTGCTCCACCATGTTGGGATCTAGATATCAATCAATCAATCTTCTTGA	18262
QY	6897	GACGTGTTGGAACGTCCTTTTTCACGATGTTCTCTCGTGGTGGGGTCCATCTTG	6956
Db	18261	GACGTGTTGGAACGTCCTTTTTCACGATGTTCTCTCGTGGTGGGGTCCATCTTG	18202
QY	6957	GGACCACTGTCGGTAGAGCATCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCAT	7016
Db	18201	GGACCACTGTCGGTAGAGCATCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCAT	18142
QY	7017	TTGTAGAAGCCATCTTCTTTTCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGGCAA	7076
Db	18141	TTGTAGAAGCCATCTTCTTTTCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGGCAA	18082
QY	7077	TGGAATCCGAGGAGTTTCCCGATATTAACCTTTGTTGAAAAGTCTCAATAGCCCTCTGG	7136
Db	18081	TGGAATCCGAGGAGTTTCCCGATATTAACCTTTGTTGAAAAGTCTCAATAGCCCTCTGG	18022
QY	7137	TCTTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAGAGTGTGCTCCACCATG	7196
Db	18021	TCTTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAGAGTGTGCTCCACCATG	17962
QY	7197	TTGGGGATCTAGATATCAATCAATCAATCAATCTTCTTGAAGAGCTGTTGGAACGCTTCT	7256
Db	17961	TTGGGGATCTAGATATCAATCAATCAATCAATCTTCTTGAAGAGCTGTTGGAACGCTTCT	17902

QY	7257	TTTTTCCAGATGTTCTCTGTTGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGCA	7316
Db	17901	TTTTTCCAGATGTTCTCTGTTGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGCA	17842
QY	7317	TCCTGAAACGATAGCTTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTT	7376
Db	17841	TCCTGAAACGATAGCTTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTT	17782
QY	7377	TCCTACTGCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCC	7436
Db	17781	TCCTACTGCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCC	17722
QY	7437	GATATTACCTTTTGTGAAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTG	7496
Db	17721	GATATTACCTTTTGTGAAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTG	17662
QY	7497	ATATTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTTGGGGATCC	7545
Db	17661	ATATTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTTGGGGATCC	17613

RESULT 6
AAA88401/c
ID AAA88401 standard; DNA; 1361 BP.
XX
AC AAA88401;
DT 09-JAN-2001 (first entry)
XX
DE 4X CaMV 35S enhancer construct.
KW CaMV; 35S; enhancer; trait-associated gene identification;
KW activation tagging; fruit; transgenic plant; ss.
OS Cauliflower mosaic virus.
FH Key Location/Qualifiers
FT repeat_region 1..1354
FT /tag= a
FT /repeat_type= TANDEM
FT /note= "4 CaMV 35S enhancer units"
FT repeat_unit 1..339
FT /tag= b
FT /note= "CaMV 35S enhancer unit 1"
FT enhancer 1..129
FT /tag= c
FT /note= "CaMV 35S enhancer AluI-EcoRV fragment"
FT enhancer 130..331
FT /tag= d
FT /note= "129 bp fragment of the CaMV sequence"
FT repeat_unit 333..339
FT /tag= e
FT /note= "additional 7 bp not associated with 35S enhancer"
FT enhancer 340..678
FT /tag= f
FT /note= "CaMV 35S enhancer unit 2"
FT enhancer 340..541
FT /tag= g
FT /note= "CaMV 35S enhancer AluI-EcoRV fragment"
FT enhancer 542..670
FT /tag= h
FT /note= "129 bp fragment of the CaMV sequence"
FT enhancer 672..678
FT /tag= i
FT /note= "additional 7 bp not associated with 35S enhancer"
FT repeat_unit 679..1017
FT /tag= j
FT /note= "CaMV 35S enhancer unit 3"
FT enhancer 679..880
FT /tag= k
FT /note= "CaMV 35S enhancer AluI-EcoRV fragment"
FT enhancer 881..1009
FT /tag= l

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FT enhancer /note= "129 bp fragment of the CamV sequence"
FT 1011..1017 /tag= m
FT /note= "additional 7 bp not associated with 35S enhancer"
FT repeat_unit 1018..1354
FT /tag= a
FT /note= "CamV 35S enhancer unit 4"
FT 1018..1219 /tag= n
FT /note= "CamV 35S enhancer AluI-EcoRV fragment"
FT 1220..1348
FT /tag= o
FT /note= "129 bp fragment of the CamV sequence"
FT 1350..1354
FT /tag= p
FT /note= "additional 6 bp not associated with 35S enhancer"
XX WO200053794-A2.
XX 14-SEP-2000.
XX 09-MAR-2000; 2000WO-US006298.
XX 12-MAR-1999; 99US-0124232P.
XX (AGRI-) AGRITOPE INC.
XX Wagner R, Mathews H, Liu XL, Waggoner WJ;
XX WPI; 2000-594336/56.
XX Identifying genes associated with a desired trait for isolating and
XX characterizing the genes comprises using an enhancer element which
XX enhances gene expression and stably integrates into the plant genome.
XX Claim 4; Fig 5; 42pp; English.
XX The present sequence is that of a 4X cauliflower mosaic virus (CaMV) 35S
XX enhancer sequence preferred for use in the method of the invention. It
XX includes 4 repeats of 202 bp AluI-EcoRV fragments of the 35S enhancer,
XX 129 bp of the CaMV sequence associated with each tandem Alu-EcoRV repeat,
XX and an additional 7 bp repeated sequence, which does not appear in the
XX 35S enhancer region of the native CaMV genome. This 4X CaMV 35S enhancer
XX element can be used in a method for identifying genes associated with a
XX desired trait in a fruit-bearing plant. The method involves: transforming
XX plant cells with an activation tagging vector comprising an element which
XX functions to enhance gene expression and has the ability to integrate
XX into the plant genome in a manner effective to enhance expression of
XX native plant genes, selecting transformed plant cells, regenerating
XX transformed plant cells to yield mature plants, selecting plants having a
XX desired trait, identifying, isolating and characterizing genes the
XX transcription of which has been enhanced, and confirming the contribution
XX of the modified expression of each identified gene to the desired trait.
XX The desired trait may be increased resistance to fungal, bacterial or
XX viral pathogens, insects, modifications in flower size, flower number,
XX flower pigmentation and shape, modified leaf number, leaf pigmentation
XX and shape, modified seed number, pattern or distribution of leaves and
XX flowers, modified stem length or between nodes, root mass or root
XX development characteristics or increased drought, salt and antibiotic
XX tolerance. Plants having short life cycles are transformed, as
XX exemplified by dwarf varieties of tomato
XX
XX Query Match 17.9%; Score 1360; DB 3; Length 1361;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-201;
XX Matches 1360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 6179 GTTTCGGATCTAGATATCATCATCAATCCACTTCTTTGAAGACGTGGTGGAAACGTCCTTC 6238
XX |||||||
XX 1360 GTTTCGGATCTAGATATCATCATCAATCCACTTCTTTGAAGACGTGGTGGAAACGTCCTTC 1301
XX |||||||
XX 6239 TTTTCCACGATGTTCTCTGCGGGTGGGGTCCATCTTTGGGACCACCTGTGCGTAGAGGC 6298
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Db 1300 TTTTCCACGATGTTCTCTGCGGGTGGGGTCCATCTTTGGGACCACCTGTGCGTAGAGGC 1241
|||
Qy 6298 ATCTTGAACGATAGCTTTCTTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTT 6358
|||
Db 1240 ATCTTGAACGATAGCTTTCTTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTT 1181
|||
Qy 6359 TTCTACTGTCCTTCGATGAAGTGCACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCC 6418
|||
Db 1180 TTCTACTGTCCTTTTCGATGAAGTGCACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCC 1121
|||
Qy 6419 CGATATTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT 6478
|||
Db 1120 CGATATTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT 1061
|||
Qy 6479 GATATTCTTGAGTAGACGAGAGTGTGCTGCTCCACCATGTTGGGATCTAGATATCACA 6538
|||
Db 1060 GATATTCTTGAGTAGACGAGAGTGTGCTGCTCCACCATGTTGGGATCTAGATATCACA 1001
|||
Qy 6539 TCAATCCACTTGTCTTTGAAGACGTGTTGGAACGTCTTTCTTTTCCAGATGTTCTCGT 6598
|||
Db 1000 TCAATCCACTTGTCTTTGAAGACGTGTTGGAACGTCTTTCTTTTCCAGATGTTCTCGT 941
|||
Qy 6599 GGGTGGGGTCCATCTTTTGGGACCACTGTCGCTAGAGGCATCTTCAACGATAGCCCTTCC 6658
|||
Db 940 GGGTGGGGTCCATCTTTTGGGACCACTGTCGCTAGAGGCATCTTCAACGATAGCCCTTCC 881
|||
Qy 6659 TTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGCTCTTTTCGATGAA 6718
|||
Db 880 TTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGCTCTTTTCGATGAA 821
|||
Qy 6719 GTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTAACCTTTGTTGAAA 6778
|||
Db 820 GTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTAACCTTTGTTGAAA 761
|||
Qy 6779 AGTCTCAATAGCCCTCTCGTCTTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAG 6838
|||
Db 760 AGTCTCAATAGCCCTCTCGTCTTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAG 701
|||
Qy 6839 AGTCTGCTGCTCCACCATGTTGGGATCTAGATATCAATCAATCACTTGTCTTTGAAGA 6898
|||
Db 700 AGTCTGCTGCTCCACCATGTTGGGATCTAGATATCAATCAATCACTTGTCTTTGAAGA 641
|||
Qy 6899 CGTGTGTGGAAGCTCTCTTTTCCAGATGTTCTCTGCTGGGTGGGGTCCATCTTTGGG 6958
|||
Db 640 CGTGTGTGGAAGCTCTCTTTTCCAGATGTTCTCTGCTGGGTGGGGTCCATCTTTGGG 581
|||
Qy 6959 ACCACTGTGCGTAGAGGCATCTTGAACGATAGCCCTTCTTTATCGCAATGATGGCATTT 7018
|||
Db 580 ACCACTGTGCGTAGAGGCATCTTGAACGATAGCCCTTCTTTATCGCAATGATGGCATTT 521
|||
Qy 7019 GTAGAAGCCATCTTCTTTCTACTGCTCTTTCGATGAAGTGCACAGATAGCTGGCAATG 7078
|||
Db 520 GTAGAAGCCATCTTCTTTCTACTGCTCTTTCGATGAAGTGCACAGATAGCTGGCAATG 461
|||
Qy 7079 GAATCCGAGGAGTGTTCGCGATATTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGCTG 7138
|||
Db 460 GAATCCGAGGAGTGTTCGCGATATTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGCTG 401
|||
Qy 7139 TTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAGAGTGTGCTGTCCACCAATGTT 7198
|||
Db 400 TTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAGAGTGTGCTGTCCACCAATGTT 341
|||
Qy 7199 GGGGATCTAGATATCAATCAATCCATCTTTCGAGACGTGGTGGAAACGTCCTTCTTTT 7258
|||
Db 340 GGGGATCTAGATATCAATCAATCCATCTTTCGAGACGTGGTGGAAACGTCCTTCTTTT 281
|||
Qy 7259 TTCCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTTGGGACCACCTGTGCGTAGAGGCATC 7318
|||
Db 280 TTCCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTTGGGACCACCTGTGCGTAGAGGCATC 221
|||
Qy 7319 TTGAAACGATAGCTTTCTTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTCTTTTC 7378
|||
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Db	220	TTGAACAGTAGCCTTTCTCTTATCCGAATGATGGCATTTGTAGAGCCATCTTCCTTTTC	161
Qy	7379	TACTGTCTCTTTTCGATGAAGTGACAGATAGCTGGGCAATCGAATCCGAGGAGTTTCCCGA	7438
Db	160	TACTGTCTCTTTTCGATGAAGTGACAGATAGCTGGGCAATCGAATCCGAGGAGTTTCCCGA	101
Qy	7439	TATTACCTCTTTGTGAAAGTCTCAATAGCCCTCTGGTCTCTCTGAGACTGTATCTTTGAT	7498
Db	100	TATTACCTCTTTGTGAAAGTCTCAATAGCCCTCTGGTCTCTCTGAGACTGTATCTTTGAT	41
Qy	7499	ATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTG	7538
Db	40	ATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTG	1
RESULT 7			
ADL71845	ADL71845 standard; DNA; 1235 BP.		
XX	AC	ADL71845;	
XX	AC		
DT	20-MAY-2004	(first entry)	
XX	XX	Arabidopsis thaliana OBP3 antisense DNA #6.	
DE	XX	Transgenic plant; Dof transcription factor; ocs binding factor;	
KW	KW	plant size; plant stature; root growth; plant; gene; ds; OBF;	
KW	KW	OBF binding protein; OBP3; SOB1; mouse-ear cross.	
XX	XX	Arabidopsis thaliana.	
OS	XX		
XX	XX	US2004045055-A1.	
PN	XX	04-MAR-2004.	
PD	XX		
PF	XX	28-AUG-2003; 2003US-00650249.	
XX	XX		
PR	XX	28-AUG-2002; 2002US-0406657P.	
XX	XX	(UNIW) UNIV WASHINGTON.	
PA	XX		
PI	XX	Neff MW;	
XX	XX		
DR	XX	WPI; 2004-225757/21.	
XX	XX		
PT	XX	New transgenic plant cell, useful in producing plants with altered size	
FT	XX	and stature and with normal and healthy root growth.	
PS	XX	Claim 37; SEQ ID NO 17; 53pp; English.	
XX	XX		
CC	XX	The invention relates to a transgenic plant transformed by a Dof	
CC	XX	transcription factor, OBF (ocs binding factor) binding protein (OBP3).	
CC	XX	OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic	
CC	XX	acid and polypeptides are useful in producing transgenic plants with	
CC	XX	altered size and stature and with normal and healthy root growth. The	
CC	XX	present sequence is Arabidopsis thaliana OBP3 antisense DNA.	
XX	XX		
SQ	XX	Sequence 1235 BP; 408 A; 222 C; 179 G; 426 T; 0 U; 0 Other;	
Query Match			
Best Local Similarity 16.3%; Score 1235; DB 12; Length 1235;			
Matches 1235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	3045	CAACCAAGACGATGACGTATATGATTTGACTTGC AAAAATAAGCAACAAATACCTGTT	3104
Db	1	CAACCAAGACGATGACGTATATGATTTGACTTGC AAAAATAAGCAACAAATACCTGTT	60
Qy	3105	CAAAATCGACACTTAATTC AAAAGGTTAGTAATAAGTAAGAGGCTTTTATTTATGAAA	3164
Db	61	CAAAATCGACACTTAATTC AAAAGGTTAGTAATAAGTAAGAGGCTTTTATTTATGAAA	120
Qy	3165	ACAAAAAGAAATAAAGAGCCCTAAGAGAAATGATGAAAAATTGAAGAGAAAAAAGAGCAATTG	3224

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RESULT 8
ADL71848
ID ADL71848 standard; DNA; 1062 BP.
XX AC ADL71848;
XX DT 20-MAY-2004 (first entry)
XX DE Arabidopsis thaliana OBP3 antisense DNA #9.
XX KW Transgenic plant; Dof transcription factor; ocs binding factor;
XX KW plant size; plant stature; root growth; plant; gene; ds; OBF;
XX KW OBF binding protein; OBP3; SOB1; mouse-ear cress.
XX OS Arabidopsis thaliana.
XX PN US2004045055-A1.
XX PD 04-MAR-2004.
XX PF 28-AUG-2003; 2003US-00650249.
XX PR 28-AUG-2002; 2002US-0406657P.
XX PA (UNITW ) UNIV WASHINGTON.
XX PI Neff MM;
XX DR WPI; 2004-225757/21.
XX PT New transgenic plant cell, useful in producing plants with altered size
XX PT and stature and with normal and healthy root growth.
XX PS Claim 40; SEQ ID NO 20; 53bp; English.
XX CC The invention relates to a transgenic plant transformed by a Dof
XX CC transcription factor, OBF (ocs binding factor) binding protein (OBP3).
XX CC OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic
XX CC acid and polypeptides are useful in producing transgenic plants with
XX CC altered size and stature and with normal and healthy root growth. The
XX CC present sequence is Arabidopsis thaliana OBP3 antisense DNA.
XX SQ Sequence 1062 BP; 348 A; 159 C; 155 G; 400 T; 0 U; 0 Other;

Query Match 14.0%; Score 1062; DB 12; Length 1062;
Best Local Similarity 100.0%; Pred. No. 5.1e-155;
Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5117 TAACTACTCAGCACTAGCTATCTTGTGATGATCTTTTGTGTTGGTGGGTTGATCTGGTG 5176
Db 1 TAACTACTCAGCACTAGCTATCTTGTGATGATCTTTTGTGTTGGTGGGTTGATCTGGTG 60
QY 5177 CTTGTTCATCGAGTTATCTCTCAGGAGATCAACCATCAGCTATATCCAAAGGCTAAT 5236
Db 61 CTTGTTCATCGAGTTATCTCTCAGGAGATCAACCATCAGCTATATCCAAAGGCTAAT 120
QY 5237 TTTTGAGGCTCAAGGAAAGGTATGGTTATAAACTATCTTTTGTGATCTTTTAAAGATCT 5296
Db 121 TTTTGAGGCTCAAGGAAAGGTATGGTTATAAACTATCTTTTGTGATCTTTTAAAGATCT 180
QY 5297 TCAAGATGTGATGATGTTTATTTGGTTGGCTTCTGGTGATATTTATGTTTATAGAAATTT 5356
Db 181 TCAAGATGTGATGATGTTTATTTGGTTGGCTTCTGGTGATATTTATGTTTATAGAAATTT 240
QY 5357 GCTCTTATATATGGCTATATATAGAGGTGGTGATATGATGATGATGATGATGATGATGAT 5416
Db 241 GCTCTTATATATGGCTATATATAGAGGTGGTGATGATGATGATGATGATGATGATGATGAT 300
QY 5417 GTTGGAAACTTTTGTGTTGTTCAATGAATATCATCGAAATCTCAATTTCTTTGGAGACC 5476
Db 301 GTTGGAACTTTTGTGTTGTTCAATGAATATCATCGAAATCTCAATTTCTTTGGAGACC 360
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QY 5477 CATTATGAGACATTGAGACATCTATAGAACATATATGTAATGTAATATAAAGCTACTTAA 5536
Db 361 CATTATGAGACATTGAGACATCTATAGAACATATATGTAATGTAATATAAAGCTACTTAA 420
QY 5537 GTCGAATTTTATGACCAAGTAAATTAATATGCGAATGTACATGCTAATATCGAGTTT 5596
Db 421 GTCGAATTTTATGACCAAGTAAATTAATATGCGAATGTACATGCTAATATCGAGTTT 480
QY 5597 AAACATATTTTCCAAATATACAACTATTTCTCTTTTCTGTCCTCAACTATATATCTTAT 5656
Db 481 AAACATATTTTCCAAATATACAACTATTTCTCTTTTCTGTCCTCAACTATATATCTTAT 540
QY 5657 CTGATTCCTTATTTCTTTTAAATTCCTTTTCTTTTCCCAAGACACAAAAAATAA 5716
Db 541 CTGATTCCTTATTTCTTTTAAATTCCTTTTCTTTTCCCAAGACACAAAAAATAA 600
QY 5717 AATCAGAAACGAAAAAAGAGATTTTAAATTCATACCCACGAGAAATATGACCTTA 5776
Db 601 AATCAGAAACGAAAAAAGAGATTTTAAATTCATACCCACGAGAAATATGACCTTA 660
QY 5777 AATTCAGACTAATCCCCCAAAATTTTCAGAAATTTATGTAATTTTTCGATTTAATAT 5836
Db 661 AATTCAGACTAATCCCCCAAAATTTTCAGAAATTTATGTAATTTTTCGATTTAATAT 720
QY 5837 TCACAAATCATATGCGCAACTAACTAATTTGAAAGACAAATGGAATGACTGAAACCATGCA 5896
Db 721 TCACAAATCATATGCGCAACTAATTTGAAAGACAAATGGAATGACTGAAACCATGCA 780
QY 5897 TAACTCTCAAGTCTCAACCTATGAAAGATCATGTAAACCAATAGACTATCATCATGATTA 5956
Db 781 TAACTCTCAAGTCTCAACCTATGAAAGATCATGTAAACCAATAGACTATCATCATGATTA 840
QY 5957 GTTAATGATGATCTATATGTAATTTCTTTTGAACATAGATATGCTAATTTATCTGGATATA 6016
Db 841 GTTAATGATGATCTATATGTAATTTCTTTTGAACATAGATATGCTAATTTATCTGGATATA 900
QY 6017 AGATGGCGTTTAACTACTTTTGCATTTTGTGTAATCTTTTCTTCTAATACATATGATC 6076
Db 901 AGATGGCGTTTAACTACTTTTGCATTTTGTGTAATCTTTTCTTCTAATACATATGATC 960
QY 6077 AATACACTTTTGTGTTTAAAGAAATTTAAAACTTTATTTCAACATCGATCATTTTTTA 6136
Db 961 AATACACTTTTGTGTTTAAAGAAATTTAAAACTTTATTTCAACATCGATCATTTTTTA 1020
QY 6137 CTTTGTGTTTCCATATGACTACATTTATAGGCTCACACTTTT 6178
Db 1021 CTTTGTGTTTCCATATGACTACATTTATAGGCTCACACTTTT 1062

RESULT 9
ADL71847
ID ADL71847 standard; DNA; 1058 BP.
XX AC ADL71847;
XX DT 20-MAY-2004 (first entry)
XX DE Arabidopsis thaliana OBP3 antisense DNA #8.
XX KW Transgenic plant; Dof transcription factor; ocs binding factor;
XX KW plant size; plant stature; root growth; plant; gene; ds; OBF;
XX KW OBF binding protein; OBP3; SOB1; mouse-ear cress.
XX OS Arabidopsis thaliana.
XX PN US2004045055-A1.
XX PD 04-MAR-2004.
XX PF 28-AUG-2003; 2003US-00650249.
XX PR 28-AUG-2002; 2002US-0406657P.
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XX (UNIW) UNIV WASHINGTON.
 XX Neff MM;
 XX WPI; 2004-225757/21.
 XX New transgenic plant cell, useful in producing plants with altered size
 PT and stature and with normal and healthy root growth.
 XX Claim 39; SEQ ID NO 19; 53pp; English.
 XX The invention relates to a transgenic plant transformed by a Dof
 CC transcription factor, OBP (ocs binding factor) binding protein (OBP3).
 CC OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic
 CC acid and polypeptides are useful in producing transgenic plants with
 CC altered size and stature and with normal and healthy root growth. The
 CC present sequence is Arabidopsis thaliana OBP3 antisense DNA.
 XX Sequence 1058 BP; 355 A; 176 C; 139 G; 388 T; 0 U; 0 Other;
 SQ Query Match 14.0%; Score 1058; DB 12; Length 1058;
 Best Local Similarity 100.0%; Pred. No. 2.1e-154;
 Matches 1058; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3045 CAACCAAGACGATGACGTATATGATGATGCTTGCAGAAATAGCAAAATACCTGTT 3104
 DB 1 CAACCAAGACGATGACGTATATGATGATGCTTGCAGAAATAGCAAAATACCTGTT 60
 QY 3105 CAAATCGACACTTAATCCAAAAGGTTAGTAATAGTAAGTAAGGCTTTTATTATGAA 3164
 DB 61 CAAATCGACACTTAATCCAAAAGGTTAGTAATAGTAAGTAAGGCTTTTATTATGAA 120
 QY 3165 ACAAAGAAATTAAGAGAGCTTAAGAGAAATGATCAAAATTTGAAAGAGAAAAAGAGCAATG 3224
 DB 121 ACAAAGAAATTAAGAGAGCTTAAGAGAAATGATCAAAATTTGAAAGAGAAAAAGAGCAATG 180
 QY 3225 TTATGAAAGAAAAAAGAGAGAGTAAAGAGAAATTAAGAAACACAATAAATTAACAA 3284
 DB 181 TTATGAAAGAAAAAAGAGAGAGTAAAGAGAAATTAAGAAACACAATAAATTAACAA 240
 QY 3285 AGGAACCTTCATTTCTCTCTTTATCCCAATTCAGCTCCCTCTCTCTCTCTCTCTCTCT 3344
 DB 241 AGGAACCTTCATTTCTCTCTTTATCCCAATTCAGCTCCCTCTCTCTCTCTCTCTCTCT 300
 QY 3345 CTCTCTCTCTAGATCAATTTCTCTCTATGATGATGATATCCACATATCTCGACC 3404
 DB 301 CTCTCTCTCTAGATCAATTTCTCTCTATGATGATGATATCCACATATCTCGACC 360
 QY 3405 TCTTACCTTAAAGGATACAAGTAAGAGATTCAGAGATGGTTTTCTCATCTCTCCAGTG 3464
 DB 361 TCTTACCTTAAAGGATACAAGTAAGAGATTCAGAGATGGTTTTCTCATCTCTCCAGTG 420
 QY 3465 AATCAGTTTCGATTCCTCAAAATTTGGCAGAGTAAAGATCAGTTTATGATATTTGCTAGAT 3524
 DB 421 AATCAGTTTCGATTCCTCAAAATTTGGCAGAGTAAAGATCAGTTTATGATATTTGCTAGAT 480
 QY 3525 GTTTCGTGATTCGTTCTCTCTCTCCCAAGTTCGATCAAGATTTATGAAATTTGATGAGA 3584
 DB 481 GTTTCGTGATTCGTTCTCTCTCTCCCAAGTTCGATCAAGATTTATGAAATTTGATGAGA 540
 QY 3585 TTTTGTTCGAAAAATTCCTAGCTATTGTGGACGCGCATATATATTACTTATGAATATTC 3644
 DB 541 TTTTGTTCGAAAAATTCCTAGCTATTGTGGACGCGCATATATATTACTTATGAATATTC 600
 QY 3645 TTAGTTGATTAACCCCTTTTTTTCTCTCTCTCGAATATACGAAATATATAAGAT 3704
 DB 601 TTAGTTGATTAACCCCTTTTTTTCTCTCTCTCGAATATACGAAATATATAAGAT 660
 QY 3705 GATTTCAATTTTGGTCTTTTTTCTTACTTCAAGACTTTTTTAAAAAATATTCTTAGTTGA 3764
 DB 661 GATTTCAATTTTGGTCTTTTTTCTTACTTCAAGACTTTTTTAAAAAATATTCTTAGTTGA 720

QY 3765 TAAACACCTTTTTTCTTCTCTCCAGGGCTTATGTATAATGTTTTTCTTACAGATT 3824
 DB 721 TAAACACCTTTTTTCTTCTCTCCAGGGCTTATGTATAATGTTTTTCTTACAGATT 780
 QY 3825 AATTTTCTCTTGGTTAGATTTTTTACACCGCCATGGAATATACATTCACAAATAAAAA 3884
 DB 781 AATTTTCTCTTGGTTAGATTTTTTACACCGCCATGGAATATACATTCACAAATAAAAA 840
 QY 3885 GTTAAAGTTACTATGACTTTAATCTGAGTTAATTTATCCATTTCTTTTTGAGCTTTGT 3944
 DB 841 GTTAAAGTTACTATGACTTTAATCTGAGTTAATTTATCCATTTCTTTTTGAGCTTTGT 900
 QY 3945 TGAAGAACTATATAATTAATCTGCAATTTCTGTCAAGTAGTCACAATTTTATCTATTTTC 4004
 DB 901 TGAAGAACTATATAATTAATCTGCAATTTCTGTCAAGTAGTCACAATTTTATCTATTTTC 960
 QY 4005 TTTTGTCTCCGACCAATGTTTCAAACTCGAATCTTTCGTTAAAAAGTTCTTTCTGCTTTA 4064
 DB 961 TTTTGTCTCCGACCAATGTTTCAAACTCGAATCTTTCGTTAAAAAGTTCTTTCTGCTTTA 1020
 QY 4065 TTATAAAGCTGAACTAATTAGTACAAATTTATGTTAAT 4102
 DB 1021 TTATAAAGCTGAACTAATTAGTACAAATTTATGTTAAT 1058

RESULT 10
 ADL71840
 ID ADL71840 standard; DNA; 888 BP.
 XX AC ADL71840;
 XX DT 20-MAY-2004 (first entry)
 XX DE Arabidopsis thaliana OBP3 antisense DNA #1.
 XX KW Transgenic plant; Dof transcription factor; ocs binding factor;
 KW plant size; plant stature; root growth; plant; gene; ds; OBF;
 KW OBF binding protein; OBP3; SOB1; mouse-ear cross.
 XX OS Arabidopsis thaliana.
 XX PN US2004045055-A1.
 XX PD 04-MAR-2004.
 XX PF 28-AUG-2003; 2003US-00650249.
 XX PR 28-AUG-2002; 2002US-0406657P.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PI Neff MM;
 XX PS Claim 26; SEQ ID NO 12; 53pp; English.
 XX DR WPI; 2004-225757/21.
 XX PT New transgenic plant cell, useful in producing plants with altered size
 PT and stature and with normal and healthy root growth.
 XX PS Claim 26; SEQ ID NO 12; 53pp; English.
 XX CC The invention relates to a transgenic plant transformed by a Dof
 CC transcription factor, OBP (ocs binding factor) binding protein (OBP3).
 CC OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic
 CC acid and polypeptides are useful in producing transgenic plants with
 CC altered size and stature and with normal and healthy root growth. The
 CC present sequence is Arabidopsis thaliana OBP3 antisense DNA.
 XX SQ Sequence 888 BP; 263 A; 193 C; 197 G; 235 T; 0 U; 0 Other;

Query Match 11.7%; Score 888; DB 12; Length 888;
 Best Local Similarity 100.0%; Pred. No. 4.1e-128;
 Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4592 TTGGCTCTCTCCAAAGCCTTGGAGATTACAAATCAAGCAACACTGGATTAGATTGGT 4651
 Db 361 TTGGCTCTCTCTCCAAAGCCTTGGAGATTACAAATCAAGCAACACTGGATTAGATTGGT 420
 QY 4652 GGAACTCAAAATAGCAACATGATAGTGGTATGAGTCTAGTGGTGGGATCTTGGATGCA 4711
 Db 421 GGAACTCAAAATAGCAACATGATAGTGGTATGAGTCTAGTGGTGGGATCTTGGATGCA 480
 QY 4712 TGGAGAACTCTCCATCAACAAGCTCAGCAATTCCTTTCTTATCAACAACACTACCGGA 4771
 Db 481 TGGAGAACTCTCCATCAACAAGCTCAGCAATTCCTTTCTTATCAACAACACTACCGGA 540
 QY 4772 TTGGTGCATCTTCAACCGGTATATCCATTTACTAGAGGTAAAGGAGGTGTTATCA 4831
 Db 541 TTGGTGCATCTTCAACCGGTATATCCATTTACTAGAGGTAAAGGAGGTGTTATCA 578
 QY 4832 GGTGATTCTCAACAGAGAGTAGTATGATTATTCATCAGCTAATGTTTAAAGCCCTTGTATG 4891
 Db 579 ----- 578
 QY 4892 GATTTTCTTCAAGCGGGGTAGCGCCAGCAAAACAGAAATGTGAAGCGGAAGAAAT 4951
 Db 579 -----AGCGGGGTAGCGCCAGCAAAACAGAAATGTGAAGCGGAAGAAAT 627
 QY 4952 GATCAGGATCGGGTAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 5011
 Db 628 GATCAGGATCGGGTAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 687
 QY 5012 AATATCAACATAAATCAAGCAGGAGCAAGGAGTACATCATGCGGAGGTAAACAGTTCT 5071
 Db 688 AATATCAACATAAATCAAGCAGGAGCAAGGAGTACATCATGCGGAGGTAAACAGTTCT 747
 QY 5072 TGGACCGGTTTCACTCCCAACAACTCAACAGGCCCTCTCTCAATTTCTAA 5119
 Db 748 TGGACCGGTTTCACTCCCAACAACTCAACAGGCCCTCTCTCAATTTCTAA 795
 RESULT 12
 ID ADI44304
 XX ADI44304 standard; DNA; 795 BP.
 XX AC ADI44304;
 XX DT 22-APR-2004 (first entry)
 XX DE Plant transcription factor related polynucleotide #1741.
 XX KW transgenic; plant; enhanced tolerance to abiotic stress;
 KW glyphosate tolerance; hormone sensitivity; disease resistance;
 KW sugar sensing; flowering; flower structure; stem bifurcation;
 KW branching pattern; apical dominance; trichome; stem morphology;
 KW root growth; root hair; seed development; cell proliferation;
 KW cell differentiation; premature senescence; necrosis; plant size;
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;
 KW transcription factor; ds.
 XX OS Unidentified.
 XX PN US2004019927-A1.
 XX PD 29-JAN-2004.
 XX PF 25-FEB-2003; 2003US-00374780.
 XX PR 18-APR-2001; 2001US-00837944.
 XX PA (SHER/) SHERMAN B K.
 PA (RIE/) RIECHMANN J L.
 PA (JIAN/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HAAR/) HAAKE V.
 PA (CREE/) CREELMAN R A.

PA (RAT/) RATCLIFFE O.
 PA (ADM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P E.
 PA (PILG/) PILGRIM M L.
 PA (DUBE/) DUBELL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 XX Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V,
 PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE,
 PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
 XX WPI; 2004-132245/13.
 XX P-PSDB; ADI44305.
 PT New transgenic plant comprising a recombinant polynucleotide of any one
 of more than 500 nucleotide sequences, useful in bioinformatic search
 methods.
 XX Disclosure; SEQ ID NO 2767; 435pp; English.
 CC The invention describes a transgenic plant comprising a recombinant
 polynucleotide of any one of more than 500 nucleotide sequences fully
 defined in the specification or its complement. The method of the
 invention can be used to produce a plant having altered traits such as:
 enhanced tolerance to abiotic stress; glyphosate tolerance; hormone
 sensitivity; disease resistance; sugar sensing; early or late flowering;
 altered flower structure, change in stem bifurcations, altered branching
 pattern, reduced apical dominance, reduced trichome density; lack of
 trichomes; reduced ectopic trichome development; altered trichome
 development; increase in trichome number; altered stem morphology;
 increased root growth; increased root hairs; altered seed development;
 altered cell proliferation or cell differentiation; rapid development;
 premature senescence; increased necrosis; increase in seedling or plant
 size; decreased plant size; leaf morphology; seed morphology; seed
 biochemistry; increase in root anthocyanins; increase in plant
 anthocyanins, or alteration in light response or shade avoidance. The
 transgenic plant, polynucleotides and polypeptides are useful in
 bioinformatic search methods. This sequence represents a plant
 transcription factor related polynucleotide.
 XX SQ Sequence 795 BP; 236 A; 180 C; 175 G; 204 T; 0 U; 0 Other;
 Query Match 9.1%; Score 692; DB 12; Length 795;
 Best Local Similarity 89.5%; Pred. No. 8.2e-98;
 Matches 795; Conservative 0; Mismatches 0; Indels 93; Gaps 1;
 QY 4232 ATGGTGGAACTGCTCGGATCGCAAAAGTCCCATTTGCTGAAGCAGCTCTAAATGGCCT 4291
 Db 1 ATGGTGGAACTGCTCGGATCGCAAAAGTCCCATTTGCTGAAGCAGCTCTAAATGGCCT 60
 QY 4292 AGATGTGACTCAACCAATCTAGTCTTCTTCAATTAATACTAGCTTACTCAACT 4351
 Db 61 AGATGTGACTCAACCAATCTAGTCTTCTTCAATTAATACTAGCTTACTCAACT 120
 QY 4352 CGCCATTTCTGCAAAACATGTCGCTGCTATTGGACACGTCGGGTTCCTTGGAGGAATGT 4411
 Db 121 CGCCATTTCTGCAAAACATGTCGCTGCTATTGGACACGTCGGGTTCCTTGGAGGAATGT 180
 QY 4412 CCTGTTGGAGGAGGCTTTAGGAGGAACAAGAGAGCAAAATCAGATCGAAATCTACGGTC 4471
 Db 181 CCTGTTGGAGGAGGCTTTAGGAGGAACAAGAGAGCAAAATCAGATCGAAATCTACGGTC 240
 QY 4472 GTGGTCTCGACTGATAATACTAGTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4531
 Db 241 GTGGTCTCGACTGATAATACTAGTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 300
 QY 4532 AACCTTAGCAAGTTTTCATAGCTACGGTCAAAATCCCGGAGTTTAAATTCCAACTTGGCCATC 4591
 Db 301 AACCTTAGCAAGTTTTCATAGCTACGGTCAAAATCCCGGAGTTTAAATTCCAACTTGGCCATC 360

KW plant resistance; viral infection resistance; maize plant;
 KW maize dwarf mosaic virus; MDMV; ds.
 XX Synthetic.

XX Key Location/Qualifiers
 FH 119..672
 FT /*tag= a
 FT /note= "Zea mays alcohol dehydrogenase 1, intron 1
 fragment"

XX W09421796-A2.

XX 29-SEP-1994.

XX 22-MAR-1994; 94WO-US003028.

XX 24-MAR-1993; 93US-00038768.

XX (PION-) PIONEER HI-BRED INT INC.
 PA (USDA) US SEC OF AGRIC.

XX Roth BA, Townsend R, McMullen MD;

XX WPI; 1994-317016/39.

XX DNA encoding maize chlorotic dwarf virus proteins - used to provide
 PT plants with resistance to the virus and related viral infections.

XX Claim 2; Page 14-17; 40pp; English.

XX This sequence shows the nucleotide sequence for the plasmid designated
 CC pPH11406. The plasmid vector contains the gene for MCDV (maize chlorotic
 CC dwarf virus) coat protein 3 placed under control of tandem cauliflower
 CC modic virus 35S promoters isolated from the 1841 strain of the virus.
 CC and a polyA signal sequence obtained from the potato proteinase inhibitor
 CC II (Pin II) gene that exhibits enhancer-like activity. The chimeric gene
 CC also includes a 79 bp sequence omega' from the 5' leader region of
 CC tobacco mosaic virus that functions as a translational enhancer; and a
 CC Zea mays alcohol dehydrogenase 1, intron 1 fragment spanning nucleotides
 CC 119-672, trimmed to 557 bp with Bal 31 nuclease, which has been shown to
 CC function as an enhancer of gene expression in monocots. The DNA is used
 CC for imparting resistance to MCDV or viruses to which MCDV infection or
 CC resistance provides cross-resistance, including maize dwarf mosaic virus
 CC strain A. Any or all of the three coat protein genes from MCDV can be
 CC used to provide protection for plants. MCDV has a single, long RNA core
 CC which is shown in AAQ74694. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 5033 BP; 1345 A; 1177 C; 1177 G; 1334 T; 0 U; 0 Other;

Query Match 8.2%; Score 621; DB 2; Length 5033;
 Best Local Similarity 95.1%; Pred. No. 8.5e-87;
 Matches 653; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

QY 6868 AGATATCATCAATCAACTGCTTTGAAGACGTGGTGGAAACGTCTCTTTTCCACGA 6927

Db 1103 AGATATCATCAATCAACTGCTTTGAAGACGTGGTGGAAACGTCTCTTTTCCACGA 1044

QY 6928 TGCTCTCGTGGGTGGGTCCATCTTGGGACCACTGTCGTAGAGCATCTTGAACGA 6987

Db 1043 TGCTCTCGTGGGTGGGTCCATCTTGGGACCACTGTCGTAGAGCATCTTGAACGA 984

QY 6988 TAGCCTTTCTTTATCGCAATGCGCATTTGTAGAAGCCATCTTCTTCTACTGTCC 7047

Db 983 TAGCCTTTCTTTATCGCAATGCGCATTTGTAGAAGCCATCTTCTTCTACTGTCC 924

QY 7048 TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 7107

Db 923 TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 864

QY 7108 TTGTGTAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTGTATTTCTTGG 7167

Db 863 TTGTGTAAAGTCTCAATAGCCCTTTGGTCTTCTGAGACTGTATCTTGTATTTCTTGG 804

QY 7168 AGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCT-----AGATATCATCAATCC 7223
 Db 803 AGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCTTTCTAGAGCATCACATCAATCC 744
 QY 7224 ACTTGCTTTGAAGACGTGGTGGAAACGTCTCTTTTCCACGATGTTCTCGTGGGTGG 7283
 Db 743 ACTTGCTTTGAAGACGTGGTGGAAACGTCTCTTTTCCACGATGTTCTCGTGGGTGG 684
 QY 7284 GGTCCATCTTTGGGACCACTGTCGTAGAGGCAATCTTGAAGATAGCCCTTTCTTTATCG 7343
 Db 683 GGTCCATCTTTGGGACCACTGTCGTAGAGGCAATCTTGAAGATAGCCCTTTCTTTATCG 624
 QY 7344 CAATGATGGCATTTGTAGAAGCCATCTTCTTCTACTGTCTTCTCGATGAAGTGACAG 7403
 Db 623 CAATGATGGCATTTGTAGGTGCCACCTTCTTCTACTGTCTTCTGATGAAGTGACAG 564
 QY 7404 ATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCTTTGTTGAAAGTCTCA 7463
 Db 563 ATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCTTTGTTGAAAGTCTCA 504
 QY 7464 ATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGTGTG 7523
 Db 503 ATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGTGTG 444
 QY 7524 TGCTCCACCATGTTGGGATCCACTAG 7550
 Db 443 TGCTCCACCATGTTGACGGATTCTTAG 417

RESULT 15

AEA40942/c
 ID AEA40942 standard; DNA; 4727 BP.

AC AEA40942;

DT 28-JUL-2005 (first entry)

DE T-DNA region of pMYL28.

KW interleukin-12; transgenic plant; Nicotiana tabacum; T-DNA; pMYL28; ds.

OS Unidentified.

XX KR2004097575-A.

XX 18-NOV-2004.

XX 12-MAY-2003; 2003KR-00029910.

XX 12-MAY-2003; 2003KR-00029910.

PA (KWON/) KWON T H.

PA (YANG/) YANG M S.

XX Kwon TH, Yang MS;

XX WPI; 2005-238941/25.

XX Production method of a large amount of biologically active interleukin-12
 PT protein using plant cell suspension culture cheaply and safely.

XX Disclosure; SEQ ID NO 2; 23pp; Korean.

XX A production method of biologically active interleukin-12 protein using
 CC plant cell suspension culture is provided, thereby cheaply and safely
 CC producing a large quantity of biologically active interleukin-12 protein.
 CC The production method of biologically active interleukin-12 protein
 CC comprises the steps of: (a) providing a transgenic plant having a gene
 CC encoding p35 subunit of interleukin-12(IL-12) and a transgenic plant
 CC having a gene encoding p40 subunit of interleukin-12(IL-12); (b) cross-
 CC breeding the p35 containing transgenic plant with the p40 containing
 CC transgenic plant to produce a transgenic plant expressing both p35 and

CC p40; (c) isolating calluses of the transgenic plant of step (b) to
CC produce a plant cell line(KTC 1021BP); and (d) suspension culturing the
CC plant cell line(KTC 1021BP) to express the biologically active
CC interleukin-12, wherein the plant is Nicotiana tabacum; gelatin may be
CC further added into the medium in step (d) for improving production of IL-
CC 12; and the IL-12 contains a signal peptide. The present sequence
CC represents T-DNA region of pMYL28.

XX
SQ Sequence 4727 BP; 1218 A; 1135 C; 1191 G; 1183 T; 0 U; 0 Other;

Query Match	8.1%;	Score 617.2;	DB 14;	Length 4727;
Best Local Similarity	93.6%;	Pred. No. 3.3e-86;		
Matches	659;	Conservative	0;	Mismatches 33; Indels 12; Gaps 1;
QY	6868	AGATATCATCAATCCACTTGTGTTGAAGACGTGGTTGGAACGTCCTTTTCCACGA	6927	
Db	3224	AGATATCATCAATCCACTTGTGTTGAAGACGTGGTTGGAACGTCCTTTTCCACGA	3165	
QY	6928	TGTTCTCTGTTGGGTGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA	6987	
Db	3164	TGCTCTCTGTTGGGTGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA	3105	
QY	6988	TAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTCTACTGTCC	7047	
Db	3104	TAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGGTGCCACCTTCTTTCTACTGTCC	3045	
QY	7048	TTTCGATGAAGTGAAGATAGTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCC	7107	
Db	3044	TTTTCGATGAAGTGAAGATAGTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCC	2985	
QY	7108	TTTGTGTAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGG	7167	
Db	2984	TTTGTGTAAGTCTCAATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTCTTGG	2925	
QY	7168	AGTAGACGAGAGTGTGTCCTCACCATGTTGGGGATCTAGATATCACATCAATCCACTT	7227	
Db	2924	AGTAGACGAGAGTGTGTCCTCACCATGTTGGGGATCTAGATATCACATCAATCCACTT	2877	
QY	7228	GCTTTGAAGACGTGTTGGAACGTCCTTTTTCACGATGTTCTCGTGGTGGGGTC	7287	
Db	2876	GCTTTGAAGACGTGTTGGAACGTCCTTTTTCACGATGTTCTCGTGGTGGGGTC	2817	
QY	7288	CATCTTTGGGACCACTGTGCGTAGAGGCATCTTGAACGATAGCCCTTCTTTATCGCAAT	7347	
Db	2816	CATCTTTGGGACCACTGTGCGCAGAGGCATCTTGAACGATAGCCCTTCTTTATCGCAAT	2757	
QY	7348	GATGGCATTTGTAGAAGCCATCTTCTTTTCTACTGTCTTTCGATGAAGTGACAGATAG	7407	
Db	2756	GATGGCATTTGTAGGTGCCACCTTCTTTTCTACTGTCTTTCGATGAAGTGACAGATAG	2697	
QY	7408	CTGGGCAATGGAATCCGAGAGGTTTCCGATATTACCCCTTTGTTGAAAAGTCTCAATAG	7467	
Db	2696	CTGGGCAATGGAATCCGAGAGGTTTCCGATATTACCCCTTTGTTGAAAAGTCTCAATAG	2637	
QY	7468	CCCTCTGGTCTTCTCAGACTGTATCTTTGATATTCTTGGAGTAGACGAGTGTGCTGCT	7527	
Db	2636	CCCTTTGGTCTTCTCAGACTGTATCTTTGATATTCTTGGAGTAGACGAGTGTGCTGCT	2577	
QY	7528	CCACCATGTTGGGGATCCACTAGTTCTAGAGCGCGCCACCGC	7571	
Db	2576	CCACCATGTTGGCAAGCTGCTTAGGCAATACGCAACCGCCTC	2533	

Search completed: December 30, 2005, 17:26:48
Job time : 2706 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.raphm** (Published_Applications_AA_Main) and **.raphn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using sw model

Run on: December 30, 2005, 17:26:56 ; Search time 470 Seconds
(without alignments)
8454.579 Million cell updates/sec

Title: US-10-650-249-1

Perfect score: 7580

Sequence: 1 agctctattaattcaagaga.....gcgccaccgcggtggagct 7580

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4172979 seqs, 262114271 residues

Total number of hits satisfying chosen parameters: 8345958

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA New:*

- 1: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubna/US05_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/1/pubna/US11_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/1/pubna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	617.2	8.1	11667	6	US-10-508-263-122
C 2	381.2	5.0	612	7	US-11-038-981A-1
C 3	379.2	5.0	1459	7	US-11-038-981A-23
C 4	377.6	5.0	3469	7	US-11-192-801-23
C 5	377.6	5.0	3754	7	US-11-192-801-15
C 6	376.2	5.0	1467	7	US-11-038-981A-21
C 7	374.6	4.9	1467	7	US-11-038-981A-22
C 8	373.6	4.9	524	7	US-11-038-981A-6
C 9	367.2	4.8	4149	7	US-11-192-801-13
C 10	303.6	4.0	835	6	US-10-391-414-10
C 11	118	1.6	1935	7	US-11-038-981A-26
C 12	116.2	1.5	332	7	US-11-038-981A-5
C 13	116.2	1.5	1273	7	US-11-038-981A-18
C 14	116.2	1.5	1281	7	US-11-038-981A-20
C 15	116.2	1.5	1935	7	US-11-038-981A-19
C 16	116.2	1.5	1935	7	US-11-038-981A-25
C 17	116.2	1.5	1939	7	US-11-038-981A-24
C 18	116.2	1.5	1963	7	US-11-038-981A-27
C 19	116.2	1.5	1963	7	US-11-038-981A-28
C 20	116.2	1.5	1971	7	US-11-038-981A-29
C 21	101.6	1.3	986	6	US-10-927-641-40
C 22	88.6	1.2	762	6	US-10-509-691-1
C 23	78.2	1.0	173602	7	US-11-121-086-25

C 24	69.2	0.9	171486	7	US-11-121-086-105	Sequence 105, Appl
C 25	68	0.9	171486	7	US-11-121-086-105	Sequence 105, Appl
C 26	66.6	0.9	173602	7	US-11-121-086-25	Sequence 25, Appl
C 27	65.8	0.9	5666	6	US-10-240-708-29	Sequence 29, Appl
C 28	65.2	0.9	5152	6	US-10-240-708-47	Sequence 47, Appl
C 29	63	0.8	49979	6	US-10-995-561-13443	Sequence 13443, A
C 30	62.6	0.8	5562	6	US-10-240-708-63	Sequence 63, Appl
C 31	62.6	0.8	105550	6	US-10-995-561-13235	Sequence 13235, A
C 32	62	0.8	8093	6	US-10-240-708-31	Sequence 31, Appl
C 33	61.6	0.8	1073	7	US-11-038-981A-16	Sequence 16, Appl
C 34	61.4	0.8	119036	6	US-10-995-561-13314	Sequence 13314, A
C 35	61.2	0.8	6317	6	US-10-240-708-11	Sequence 11, Appl
C 36	60.8	0.8	20317	6	US-10-995-561-13460	Sequence 13460, A
C 37	60.6	0.8	6306	6	US-10-240-708-50	Sequence 50, Appl
C 38	60.2	0.8	20317	6	US-10-995-561-13460	Sequence 38, Appl
C 39	59.6	0.8	5501	6	US-10-240-708-38	Sequence 20, Appl
C 40	59.6	0.8	6866	6	US-10-240-708-20	Sequence 2, Appl
C 41	59.4	0.8	240	7	US-11-038-981A-2	Sequence 2, Appl
C 42	59.4	0.8	1176	7	US-11-038-981A-11	Sequence 11, Appl
C 43	59.4	0.8	1184	7	US-11-038-981A-9	Sequence 9, Appl
C 44	59.4	0.8	1184	7	US-11-038-981A-10	Sequence 10, Appl
C 45	59	0.8	125	7	US-11-038-981A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-10-508-263-122/c

; Sequence 122, Application US/10508263

; GENERAL INFORMATION:

; APPLICANT: BASF Plant Science GmbH

; TITLE OF INVENTION: Constructs and methods for regulating gene expression

; FILE REFERENCE: 53262-20085.00

; CURRENT APPLICATION NUMBER: US/10/508,263

; CURRENT FILING DATE: 2004-09-20

; NUMBER OF SEQ ID NOS: 126

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 122

; LENGTH: 11667

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Description of the artificial sequence: suppression

; OTHER INFORMATION: construct 2 p3300.1-Toc159-GFP-RNAi

US-10-508-263-122

Query Match	8.1%	Score 617.2;	DB 6;	Length 11667;
Best Local Similarity	93.6%	Pred. No. 1.4e-96;		
Matches	659;	Conservative	0;	Mismatches 33;
				Indels 12;
				Gaps 1;
Qy	6868	AGATATACATCAATCCACTTGTCTTGAAGACGTGGTTGGAAACGCTCTCTTTTCCACGA	6927	
Db	1112	AGATATACATCAATCCACTTGTCTTGAAGACGTGGTTGGAAACGCTCTCTTTTCCACGA	1053	
Qy	6928	TGTTCTCTCGTGGGTGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCATCTTGAACGA	6987	
Db	1052	TGCTCTCTCGTGGGTGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCATCTTGAACGA	993	
Qy	6988	TAGCCTTCTCTTATCGCAATGATGGCAATTTGTAGAAGCCATCTCTTCTACTGTCC	7047	
Db	992	TAGCCTTCTCTTATCGCAATGATGGCAATTTGTAGGTGCCACCTTCTTCTACTGTCC	933	
Qy	7048	TTTCGATCAAGTCAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC	7107	
Db	932	TTTGTATGAAGTACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC	873	
Qy	7108	TTTGTGTAAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATATTCTGG	7167	
Db	872	TTTGTGTAAAAGTCTCAATAGCCCTTGTGCTCTTCTGAGACTGTATCTTTGATATTCTGG	813	
Qy	7168	AGTAGAGAGAGTGTGCTGCTCCACCATGTTGGGATCTAGATATCATCATCAATCCATT	7227	

Db 812 AGTAGACGAGAGTGTCTGCTCCACCATGT-----TATCATCATCAATCCACTT 765
Qy 7228 GCTTTGAAGACGTGGTTGGAACGTCTCTTTTCCACGATGTTCTCGTGGGTGGGGTC 7287
Db 764 GCTTTGAAGACGTGGTTGGAACGTCTCTTTTCCACGATGCTCTCGTGGGTGGGGTC 705
Qy 7288 CATCTTTGGGACCACTGTCTGGTAGAGGCATCTTGAACGATAGCCCTTTCCTTTATCGCAAT 7347
Db 704 CATCTTTGGGACCACTGTCTGGCAGAGGCATCTTGAACGATAGCCCTTTCCTTTATCGCAAT 645
Qy 7348 GATGSCATTTGTAGAAGCCATCTCTCTTTTCTACTGTCTCTTTCGATGAAGTGACAGATAG 7407
Db 644 GATGSCATTTGTAGTGTCCACCTCTCTCTTTCTACTGTCTCTTTCGATGAAGTGACAGATAG 585
Qy 7408 CTGGSCAATGGAATCCGAGGAGTTTCCCGATATTTACCTTTTGTGAAAAGTCTCAATAG 7467
Db 584 CTGGSCAATGGAATCCGAGGAGTTTCCCGATATTTACCTTTTGTGAAAAGTCTCAATAG 525
Qy 7468 CCTCTGTCTTCTGAGACTGTATCTTTTGATATTTCTTGAGTAGACGAGAGTGTCTGCT 7527
Db 524 CCTTTGTCTTCTGAGACTGTATCTTTTGATATTTCTTGAGTAGACGAGAGTGTCTGCT 465
Qy 7528 CCACCATCTTGGGATCCACTAGTTCTTAGAGCGGCCGCCACGC 7571
Db 464 CCACCATCTTGGCAAGCTGCTCTAGCCAATAGCCAAACCGCTC 421

RESULT 2

US-11-038-981A-1/c

; Sequence 1, Application US/11038981A

; Publication No. US20050283856A1

; GENERAL INFORMATION:

; APPLICANT: Conner, Timothy W.

; APPLICANT: Flasiński, Stanisław

; APPLICANT: Pang, Sheng Z

; APPLICANT: You, Jinsong

; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS

; FILE REFERENCE: 38-21(51446)B

; CURRENT APPLICATION NUMBER: US/11/038,981A

; CURRENT FILING DATE: 2005-01-20

; PRIOR APPLICATION NUMBER: 60/537,793

; PRIOR FILING DATE: 2004-01-20

; NUMBER OF SEQ ID NOS: 35

; SEQ ID NO 1

; LENGTH: 612

; TYPE: DNA

; ORGANISM: Cauliflower mosaic virus

US-11-038-981A-1

Query Match 5.0%; Score 381.2; DB 7; Length 612;
Best Local Similarity 81.5%; Pred. No. 1.2e-56;
Matches 489; Conservative 0; Mismatches 33; Indels 78; Gaps 1;

Qy 6190 AGATATCATCAATCCACTTGTGAGAGCGTGGTTGGAACGTCCTTTTCCACGA 6249
Db 526 AGATATCATCAATCCACTTGTGAGAGCGTGGTTGGAACGTCCTTTTCCACGA 467
Qy 6250 TGTCTCTGTGGGTGGGGTCCATCTTTGGGACCACTGTCTGGTAGAGGCATCTTGAACGA 6309
Db 466 TGTCTCTGTGGGTGGGGTCCATCTTTGGGACCACTGTCTGGTAGAGGCATCTTGAACGA 407
Qy 6310 TAGCCCTTTCTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTTCTACTGTCC 6369
Db 406 TGGCCCTTTCTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTTCTACTGTCT 347
Qy 6370 TTTGATGAAGTGACAGATAGTGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 6429
Db 346 TCACAATAAAGTGACAGATAGTGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 287
Qy 6430 TTTGTTGAAAAGTCTCAATAGCCCTGTGTCTTCTGAGACTGTATCTTTTGATATTCTTGG 6489
Db 286 TTTGTTGAAAAGTCTCAATCGGAC-----CATCGACCA 263

Qy 6490 AGTAGACGAGAGTGTCTGCTCCACCATGTGGGGATCTAGATATCATCAATCCACTT 6549
Db 262 -----CATCATCAATCCACTT 245
Qy 6550 GCTTTGAAGACGTGGTTGGAACGTCTTTTCCACGATGTTCTCGTGGGTGGGGTC 6609
Db 244 GCTTTGAAGACGTGGTTGGAACGTCTTTTCCACGATGCTCTCGTGGGTGGGGTC 185
Qy 6610 CATCTTTGGGACCACTGTCTGGTAGAGGCATCTTGAACGATAGCCCTTTCCTTTATCGCAAT 6669
Db 184 CATCTTTGGGACCACTGTCTGGCAGAGGCATCTTCAACGATGGCCCTTTCCTTTATCGCAAT 125
Qy 6670 GATGSCATTTGTAGAAGCCATCTTCTCTTCTACTGTCTCTTTCGATGAAGTGACAGATAG 6729
Db 124 GATGSCATTTGTAGAGCCACTTCTCTTTTCCACTATCTTCACAATAAAGTGACAGATAG 65
Qy 6730 CTGGGCAATGGAATCCGAGGAGTTTCCCGATATTTACCTTTTGTGAAAAGTCTCAATAG 6789
Db 64 CTGGGCAATGGAATCCGAGGAGTTTCCCGATATTTACCTTTTGTGAAAAGTCTCAATCG 5

RESULT 3

US-11-038-981A-23/c

; Sequence 23, Application US/11038981A

; Publication No. US20050283856A1

; GENERAL INFORMATION:

; APPLICANT: Conner, Timothy W.

; APPLICANT: Flasiński, Stanisław

; APPLICANT: Pang, Sheng Z

; APPLICANT: You, Jinsong

; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS

; FILE REFERENCE: 38-21(51446)B

; CURRENT APPLICATION NUMBER: US/11/038,981A

; CURRENT FILING DATE: 2005-01-20

; PRIOR APPLICATION NUMBER: 60/537,793

; PRIOR FILING DATE: 2004-01-20

; NUMBER OF SEQ ID NOS: 35

; SEQ ID NO 23

; LENGTH: 1459

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Artificial promoter sequence

US-11-038-981A-23

Query Match 5.0%; Score 379.2; DB 7; Length 1459;
Best Local Similarity 80.4%; Pred. No. 3.6e-56;
Matches 492; Conservative 0; Mismatches 43; Indels 77; Gaps 1;

Qy 6174 CTTTGTGTTTCGGATCTAGATATCATCAATCCACTTGTGAGAGCGTGGTTGGAACG 6233
Db 1319 CTTTGAAGACGGAGGAGGATCATCAATCCACTTGTGTAAGACGTGGTTGGAACG 1260
Qy 6234 TCTTCTTTTCCACGATGTTCTCTGTGGTGGGGTCCATCTTTGGGACCACTGTCTGCTA 6293
Db 1259 TCTTCTTTTCCACGATGTTCTCTGTGGTGGGGTCCATCTTTGGGACCACTGTCTGCTA 1200
Qy 6294 GAGGCATCTTGAACGATAGCCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCACT 6353
Db 1199 GAGGCATCTTCAACGATGGCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCACT 1140
Qy 6354 TCCTTTTCTACTGTCTTTTCGATGAAGTGACAGATAGTGGCAATGGAATCCGAGGAGG 6413
Db 1139 TCCTTTTCCACTATCTTCACAATAAAGTGACAGATAGTGGCAATGGAATCCGAGGAGG 1080
Qy 6414 TTTCCCGATATTACCTTTTGTGAAAAGTCTCAATAGCCCTCTGTCTTCTCTGAGACTGTA 6473
Db 1079 TTTCCCGATATTACCTTTTGTGAAAAGTCTCA----- 1047
Qy 6474 TCTTTGATATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGAGTCTAGATA 6533
Db 1046 -----CATCGACCA 1037

FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-22

Query Match 4.9%; Score 374.6; DB 7; Length 1467;
Best Local Similarity 81.3%; Pred. No. 2.2e-55;
Matches 482; Conservative 0; Mismatches 34; Indels 77; Gaps 1;
QY 6193 TATCATCAATCCACTTCTGTTGAAGACGTTGGTGAACGTCCTTTTCCACGATGT 6252
DB 926 TATCATCAATCCACTTCTGTTGAAGACGTTGGTGAACGTCCTTTTCCACGATGC 867
QY 6253 TCCTCGTGGGTGGGGTCCATCTTTGGACCACTGTCGGCAGAGCATCTTCAACGATAG 6312
DB 866 TCCTCGTGGGTGGGGTCCATCTTTGGACCACTGTCGGCAGAGCATCTTCAACGATGG 807
QY 6313 CTTTCTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCCTTTCTACTGTCCTTT 6372
DB 806 CTTTCTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCCTTTCTACTGTCCTTT 747
QY 6373 CGATGAAGTGACAGATAGCTGGCAATGGAATCCGAGGAGTTTCCCGATATTACCCCTTT 6432
DB 746 CAATAAAGTGACAGATAGCTGGCAATGGAATCCGAGGAGTTTCCCGATATTACCCCTTT 687
QY 6433 GTTGAAGAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATATTCTTGGAGT 6492
DB 686 GTTGAAGAGTCTCA----- 673
QY 6493 AGACGAGAGTGTGCTGCTCCACCATGTTGGGATCTAGATATCATCAATCCACTTGCCT 6552
DB 672 -----CATCGGACCATCATCAATCCACTTGCCT 644
QY 6553 TTGAAGACGTTGGTGAACGTCCTTTTCCACGATGTTCTCGTGGGTGGGGTCCCAT 6612
DB 643 TTGAAGACGTTGGTGAACGTCCTTTTCCACGATGTTCTCGTGGGTGGGGTCCCAT 584
QY 6613 CTTTGGGACCACTGTCGGTAGAGGATCTTGAACGATAGCCCTTCTTTATCGCAATGAT 6672
DB 583 CTTTGGGACCACTGTCGGTAGAGGATCTTGAACGATAGCCCTTCTTTATCGCAATGAT 524
QY 6673 GGCATTTCTAGAAGCCATCTTCTCTTCTACTGTCCTTTCCGATGAAGTGACAGATAGCTG 6732
DB 523 GGCATTTCTAGAAGCCATCTTCTCTTCTACTGTCCTTTCCGATGAAGTGACAGATAGCTG 464
QY 6733 GGCATGAATCCGAGGAGTTTCCGATATTACCCCTTTGTTGAAAAGTCTCA 6785
DB 463 GGCATGAATCCGAGGAGTTTCCGATATTACCCCTTTGTTGAAAAGTCTCA 411

RESULT 8
US-11-038-981A-6/c
; Sequence 6, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038, 981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 6
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-11-038-981A-6

Query Match 4.9%; Score 373.6; DB 7; Length 524;
Best Local Similarity 81.2%; Pred. No. 2.4e-55;

Matches 481; Conservative 0; Mismatches 34; Indels 77; Gaps 1;
QY 6194 ATCATCAATCCACTTCTGTTGAAGACGTTGGTGAACGTCCTTTTCCACGATGTT 6253
DB 524 ATCATCAATCCACTTCTGTTGAAGACGTTGGTGAACGTCCTTTTCCACGATGCT 465
QY 6254 CCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGATCTTGAACGATAGC 6313
DB 464 CCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGCAGAGGATCTTCAACGATGGC 405
QY 6314 CTTTCTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTCTTTTCTACTGTCCTTTTC 6373
DB 404 CTTTCTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTCTTTTCTACTGTCCTTTTC 345
QY 6374 GATGAAGTGACAGATAGCTGGCAATGGAATCCGAGGAGTTTCCCGATATTACCCCTTTG 6433
DB 344 AATAAAGTGACAGATAGCTGGCAATGGAATCCGAGGAGTTTCCCGATATTACCCCTTTG 285
QY 6434 TTGAAGAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTA 6493
DB 284 TTGAAGAGTCTCA----- 272
QY 6494 GACGAGAGTGTGCTGCTCCACCATGTTGGGATCTAGATATCATCAATCCACTTGCCTT 6553
DB 271 -----CATCGGACCATCATCAATCCACTTGCCTT 242
QY 6554 TGAAGACGTTGGTGAACGTCCTTTTCCACGATGTTCTCGTGGGTGGGGTCCATC 6613
DB 241 TGAAGACGTTGGTGAACGTCCTTTTCCACGATGTTCTCGTGGGTGGGGTCCATC 182
QY 6614 TTTGGGACCACTGTCGGTAGAGGATCTTGAACGATAGCCCTTCTTTATCGCAATGATG 6673
DB 181 TTTGGGACCACTGTCGGTAGAGGATCTTGAACGATAGCCCTTCTTTATCGCAATGATG 122
QY 6674 GCATTTGTAGAAGCCATCTTCTCTTCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGG 6733
DB 121 GCATTTGTAGAAGCCATCTTCTCTTCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGG 62
QY 6734 GCAATGAATCCGAGGAGTTTCCGATATTACCCCTTTGTTGAAAAGTCTCA 6785
DB 61 GCAATGAATCCGAGGAGTTTCCGATATTACCCCTTTGTTGAAAAGTCTCA 10

RESULT 9
US-11-192-801-13/c
; Sequence 13, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 4149
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette
; FEATURE:
; NAME/KEY: Promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; FEATURE:
; NAME/KEY: intron
; LOCATION: (669)..(1472)

OTHER INFORMATION: I-Zm.Hsp70
FEATURE:
NAME/KEY: transit_peptide
LOCATION: (1489)..(1635)
OTHER INFORMATION: amino terminal TS-Zm.rbcS
FEATURE:
NAME/KEY: intron
LOCATION: (1636)..(1798)
OTHER INFORMATION: I-Zm.rbcS
FEATURE:
NAME/KEY: transit_peptide
LOCATION: (1799)..(1885)
OTHER INFORMATION: carboxy terminus TS-Zm.rbcS
FEATURE:
NAME/KEY: CDS
LOCATION: (1885)..(3843)
OTHER INFORMATION: Cry3Bb1 variant v11231
FEATURE:
NAME/KEY: terminator
LOCATION: (3871)..(4127)
OTHER INFORMATION: T-AGRu.nos 3' transcription termination and
OTHER INFORMATION: polyadenylation sequence
US-11-192-801-13

Query Match 4.8%; Score 367.2; DB 7; Length 4149;
Best Local Similarity 81.4%; Pred. No. 5.5e-54;
Matches 485; Conservative 0; Mismatches 33; Indels 78; Gaps 2;
QY 6190 AGATATCACATCAATCCACTTGTCTTTGAAGACGTGGTGGAAACGCTCTCTTTTCCACGA 6249
DB 552 AGATATCACATCAATCCACTTGTCTTTGAAGACGTGGTGGAAACGCTCTCTTTTCCACGA 493
QY 6250 TGTTCCTCGTGGTGGGGTGCATCTTTGGACCACTGCTGGTAGAGGATCTTGAACGA 6309
DB 492 TGTCTCTCGTGGTGGGGTGCATCTTTGGACCACTGCTGGTAGAGGATCTTGAACGA 433
QY 6310 TAGCCCTTCCCTTATCGCAATGATGGCATTTCTAGAAGCCATCTCTCTTTCTACTGTCC 6369
DB 432 TGGCCCTTCTTATCGCAATGATGGCATTTGTAGGAGCCACTCTCTCTTTCTACTGTCT 374
QY 6370 TTTCATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 6429
DB 373 TCACATTAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 314
QY 6430 TTGTGTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATCTTTGG 6489
DB 313 TTGTGTGAAAGTCTCA----- 297
QY 6490 AGTAGACGAGTGTGCTGCTCCACCATGTTGGGATCTAGATATCACATCAATCCACTT 6549
DB 296 -----CATCGACCATCACATCAATCCACTT 271
QY 6550 GCTTTGAAGACGTGGTGGAAAGTCTCTTTTTCACGATGTTCTCGTGGTGGGGTCC 6609
DB 270 GCTTTGAAGACGTGGTGGAAAGTCTCTTTTTCACGATGTTCTCGTGGTGGGGTCC 211
QY 6610 CATCTTTGGGACCACTGCTGGTAGAGGATCTTGAACGATAGCCCTTCTTTATCGCAAT 6669
DB 210 CATCTTTGGGACCACTGCTGGTAGAGGATCTTGAACGATAGCCCTTCTTTATCGCAAT 151
QY 6670 GATGGCATTTGTAAGGACCATCTCTTTTCTACTGTCTTTCGATGAAGTGACAGATAG 6729
DB 150 GATGGCATTTGTAAGGACCACTCTCTTTTCTACTGTCTTTCGATGAAGTGACAGATAG 91
QY 6730 CTGGCAATGGAATCCGAGGAGGTTTCCGATATTACCCCTTTGTTGAAAGTCTCA 6785
DB 90 CTGGCAATGGAATCCGAGGAGGTTTCCGATATTACCCCTTTGTTGAAAGTCTCA 35

RESULT 10
US-10-391-414-10/c
; Sequence 10, Application US/10391414
; Publication No. US20050278799A1

GENERAL INFORMATION:
; APPLICANT: SHINOZAKI, Kazuko
; APPLICANT: KATSURA, Koji
; APPLICANT: ITO, Yusuke
; TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
; FILE REFERENCE: 382.1041
; CURRENT APPLICATION NUMBER: US/10/391.414
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: JP 2002-377316
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 835
; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-10-391-414-10

Query Match 4.0%; Score 303.6; DB 6; Length 835;
Best Local Similarity 91.7%; Pred. No. 2.5e-43;
Matches 321; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 7207 AGATATCACATCAATCCACTTGTCTTTGAAGACGTGGTGGAAACGCTCTCTTTTCCACGA 7266
DB 744 AGATATCACATCAATCCACTTGTCTTTGAAGACGTGGTGGAAACGCTCTCTTTTCCACGA 685
QY 7267 TGTTCCTCGTGGTGGGGTGCATCTTTGGACCACTGCTGGTAGAGGATCTTTGAACGA 7326
DB 684 TGCTCCTCGTGGTGGGGTGCATCTTTGGACCACTGCTGGTAGAGGATCTTTGAACGA 625
QY 7327 TAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTCC 7386
DB 624 TGGCCTTTCTTTATCGCAATGATGGCATTTGTAGAGGCCACTTCTTTTCCACTATCT 565
QY 7387 TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 7446
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QY 7447 TTGTGTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATCTTTGG 7506
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QY 7507 AGTAGACGAGTGTGCTGCTCCACCATGTTGGGATCCACTAGTCTTAG 7556
DB 444 AGTAGACGAGTGTGCTGCTCCACCATGTTGACGAGATTTTCTTCTTG 395

RESULT 11
US-11-038-981A-26
; Sequence 26, Application US/11038981A
; Publication No. US20050283856A1
GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Flasiński, Stanislaw
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038.981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 26
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-26

Query Match 1.6%; Score 118; DB 7; Length 1935;
Best Local Similarity 78.0%; Pred. No. 1.8e-11;


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; APPLICANT: Flasiński, Stanisław
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 19
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-19

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Best Local Similarity 97.5%; Pred No. 3.2e-11;
Matches 118; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      524 AGATATCACATCAATCCACTTGGCTTTGAAGACGTGGTTGGAAACGTCTTTTTCACGA 465

QY      6250 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACCTGTCGGTAGAGGCATCTTGAACGA 6309
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Db      464 TGCTCCTCGTGGGTGGGGTCCATCTTTGGGACCACCTGTCGGCAGAGGCATCTTCAACGA 405

QY      6310 T 6310
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Job time : 477 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 30, 2005, 16:41:57 ; Search time 3569 Seconds
(without alignments)
17562.871 Million cell updates/sec

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Perfect score: 7580
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_Main:
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2: /cgn2_6/prodata/1/pubpna/us08_PUBCOMB.seq.*
3: /cgn2_6/prodata/1/pubpna/us09A_PUBCOMB.seq.*
4: /cgn2_6/prodata/1/pubpna/us09B_PUBCOMB.seq.*
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10: /cgn2_6/prodata/1/pubpna/us11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1730	22.8	1746	7	US-10-650-249-18
3	1402.4	18.5	10078	5	US-10-033-190-3
4	1360	17.9	1361	3	US-09-522-334-1
5	1235	16.3	1235	7	US-10-650-249-17
6	1062	14.0	1062	7	US-10-650-249-20
7	1058	14.0	1058	7	US-10-650-249-19
8	888	11.7	888	7	US-10-650-249-12
9	692	9.1	795	6	US-10-225-066A-409
10	692	9.1	795	7	US-10-374-780A-2767
11	692	9.1	795	9	US-10-225-066A-409
12	684	9.0	684	7	US-10-650-249-15
13	617.2	8.1	8428	6	US-10-161-403-90
14	617.2	8.1	8428	8	US-10-161-408-2
15	617.2	8.1	8428	10	US-11-006-076-90
16	617.2	8.1	10122	6	US-10-161-403-97
17	617.2	8.1	10122	8	US-10-161-408-8
18	617.2	8.1	10122	10	US-11-006-076-97
19	617.2	8.1	10549	6	US-10-161-403-92
20	617.2	8.1	10549	8	US-10-161-408-3
21	617.2	8.1	10549	10	US-11-006-076-92
22	617.2	8.1	11182	6	US-10-161-403-89
23	617.2	8.1	11182	8	US-10-161-408-1

24	617.2	8.1	11182	10	US-11-006-076-89	Sequence 89, Appl
25	617.2	8.1	11478	9	US-10-473-945-2	Sequence 2, Appl
c 26	617.2	8.1	12304	9	US-10-473-945-5	Sequence 5, Appl
27	617.2	8.1	12497	9	US-10-473-945-4	Sequence 4, Appl
28	617.2	8.1	12592	6	US-10-161-403-95	Sequence 95, Appl
29	617.2	8.1	12592	8	US-10-161-408-6	Sequence 6, Appl
30	617.2	8.1	12592	10	US-11-006-076-95	Sequence 95, Appl
31	617.2	8.1	14627	6	US-10-161-403-109	Sequence 109, Appl
32	617.2	8.1	14627	8	US-10-161-408-21	Sequence 21, Appl
33	617.2	8.1	14627	10	US-11-006-076-109	Sequence 109, Appl
c 34	616.8	8.1	829	5	US-10-109-812-10	Sequence 10, Appl
c 35	615	8.1	5475	9	US-10-473-945-1	Sequence 1, Appl
c 36	614.6	8.1	1334	6	US-10-322-656-12	Sequence 12, Appl
c 37	611.8	8.1	1216	9	US-10-473-945-3	Sequence 3, Appl
c 38	599.6	7.9	11182	6	US-10-161-403-89	Sequence 89, Appl
c 39	599.6	7.9	11182	8	US-10-161-408-1	Sequence 1, Appl
c 40	599.6	7.9	11182	10	US-11-006-076-89	Sequence 89, Appl
c 41	599.6	7.9	12592	6	US-10-161-403-95	Sequence 95, Appl
c 42	599.6	7.9	12592	8	US-10-161-408-6	Sequence 6, Appl
c 43	599.6	7.9	12592	10	US-11-006-076-95	Sequence 95, Appl
c 44	599.6	7.9	14627	6	US-10-161-403-109	Sequence 109, Appl
c 45	599.6	7.9	14627	8	US-10-161-408-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-650-249-1
; Sequence 1, Application US/10650249
; Publication No. US20040045055A1
; GENERAL INFORMATION:
; APPLICANT: Nseff, Michael M
; TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
; FILE REFERENCE: WSHU 2064.1
; CURRENT APPLICATION NUMBER: US/10/650,249
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,657
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-1

Query Match	100.0%	Score	7580	DB	7	Length	7580
Best Local Similarity	100.0%	Pred. No.	0				
Matches	7580	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
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DB	1	AGCTCTATTATTTCAGAGAGCAGCAATAAAGCAAACTCAAAACCTTAAGTTTCTGA	60				
QY	61	ATATCAAAAGGGGTAGATAATCATTTCTCTCAACTAGTTTAAAAAAGTATGATAAATTA	120				
DB	61	ATATCAAAAGGGGTAGATAATCATTTCTCTCAACTAGTTTAAAAAAGTATGATAAATTA	120				
QY	121	AAAAACAATGGATCAATTAAGAGACAGTAGTTTATGATATATATGTTGGGATCGATTA	180				
DB	121	AAAAACAATGGATCAATTAAGAGACAGTAGTTTATGATATATATGTTGGGATCGATTA	180				
QY	181	GTTCATCATCAAAAGATCAAAATATGACCGGTATTCGCCAAATACCAAGCGCAAT	240				
DB	181	GTTCATCATCAAAAGATCAAAATATGACCGGTATTCGCCAAATACCAAGCGCAAT	240				
QY	241	CATCGGATTTCAAAACACCTTAATGCTCATTTCAAAATCTATACTAATCTCTCAATTA	300				
DB	241	CATCGGATTTCAAAACACCTTAATGCTCATTTCAAAATCTATACTAATCTCTCAATTA	300				
QY	301	CAAAGCTAGTAGATTTTCTCAAGTGAGCAACAGTCTAATTTCTTCTGAAAAAATTTGT	360				

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7201 GGATCTAGATATACATCAATCCACTTGTCTTTGAAGACGTGGTTGGAACTCTCTCTTTT 7260
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RESULT 2
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; Sequence 18, Application US/10650249
; Publication No. US20040045055A1
; GENERAL INFORMATION:
; APPLICANT: Neff, Michael M
; TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
; TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
; FILE REFERENCE: WSHU 2064.1
; CURRENT APPLICATION NUMBER: US/10/650,249
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,657
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-18

Query Match 22.8%; Score 1730; DB 7; Length 1746;
Best Local Similarity 99.8%; Pred. No. 3.9e-305;

Matches 1743; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
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DB 1 AACAGAGAGAAATCCAGATCGAAATCTACGGTCGTGGTCTCGACTGATTAATCTACT 60
QY 4496 AGTACTCTCATCTTACTTCTCGCCCAAGTTACTCAAAACCCCTAGCAAGTTTTCATAGCTAC 4555
DB 61 AGTACTCTCATCTTACTTCTCGCCCAAGTTACTCAAAACCCCTAGCAAGTTTTCATAGCTAC 120
QY 4556 GGTCAAAATCCCGAGTTTAAATTCCAACTTTCGCCCATCTTTCGCCCTCTCTCCAAAGCCCTTGA 4615
DB 121 GGTCAAAATCCCGAGTTTAAATTCCAACTTTCGCCCATCTTTCGCCCTCTCTCCAAAGCCCTTGA 180
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DB 181 GATTAACAATCAAGCAACACATCTGGATTTAGATTTTGGTGGAACTCAAAATAGCAACATGATA 240
QY 4676 AGTGTATGAGTTCTAGTGGTGGGATCTTGGATGATGGAGAAATACCTCCATCAACAAC 4735
DB 241 AGTGTATGAGTTCTAGTGGTGGGATCTTGGATGATGGAGAAATACCTCCATCAACAAC 300
QY 4736 GCTCAGCAATTCCTTTCTTGATCAACACTACCGGATTTGGTCAATCTTCAAAACGCTTGA 4795
DB 301 GCTCAGCAATTCCTTTCTTGATCAACACTACCGGATTTGGTCAATCTTCAAAACGCTTGA 360
QY 4796 TATCATTTACTAGAAAGTAAAGGAGTGTAAATCAAGTGATTTCAACAGAAAGTGTAGT 4855
DB 361 TATCATTTACTAGAAAGTAAAGGAGTGTAAATCAAGTGATTTCAACAGAAAGTGTAGT 420
QY 4856 GATTAATTCATCAGCTAATGTTTAAAGCCTTGATGGATTTTCTTCAGGCGGGGTAGC 4915
DB 421 GATTAATTCATCAGCTAATGTTTAAAGCCTTGATGGATTTTCTTCAGGCGGGGTAGC 480
QY 4916 GCCCGCAACAAAGAAATGTGAAGCGGAAGAAATGATCAGGATCGGGGTAGGATGG 4975
DB 481 GCCCGCAACAAAGAAATGTGAAGCGGAAGAAATGATCAGGATCGGGGTAGGATGG 540
QY 4976 GATGAGTGAATTAATCAAGAAATCTTTTGGGTAATATCAACATAAACTCAGGCAG 5035
DB 541 GATGAGTGAATTAATCAAGAAATCTTTTGGGTAATATCAACATAAACTCAGGCAG 600
QY 5036 AACGAGGAATACATCATGCGGAGGTAAACAGTCTTGGACCGGTTTCACTTCCAAACAAC 5095
DB 601 AACGAGGAATACATCATGCGGAGGTAAACAGTCTTGGACCGGTTTCACTTCCAAACAAC 660
QY 5096 TCAACAGGCCATCTCTCATTC--TAAGTACTCAGCACTAGCTATTTCTTGATGATTTCTTT 5152
DB 661 TCAACAGGCCATCTCTCATTTAATAAGTACTCAGCACTAGCTATTTCTTGATGATTTCTTT 720
QY 5153 TGTGTTGGGGTGTACATTTGGTGTCTGTCGCGAGTTATTTGTCGAGGAAGATCAAAAC 5212
DB 721 TGTGTTGGGGTGTACATTTGGTGTCTGTCGCGAGTTATTTGTCGAGGAAGATCAAAAC 780
QY 5213 ATGCACTATATCCAAAGGCTAAATTTGAGGCTCAAGGCTCAAGGAAAGGATGTTGTTATAAATA 5272
DB 781 ATGCACTATATCCAAAGGCTAAATTTGAGGCTCAAGGAAAGGATGTTGTTATAAATA 840
QY 5273 TCTTTTGTATCTTTTAAAGATCTTCAAGTGTAGTATGTTTATTTGGTGGCTTCTGCT 5332
DB 841 TCTTTTGTATCTTTTAAAGATCTTCAAGTGTAGTATGTTTATTTGGTGGCTTCTGCT 900
QY 5333 GATATTTATGTTTATTAAGATTTTGGTCTTATATATATATATATATATAGAGGTGGGGTG 5392
DB 901 GATATTTATGTTTATTAAGATTTTGGTCTTATATATATATATATATATAGAGGTGGGGTG 960
QY 5393 ATATGATGAATCAAGAGTGTGAACTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5452
DB 961 ATATGATGAATCAAGAGTGTGAACTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1020
QY 5453 CGAATTTCTCAATTTCTGGAGACCCATATGAGACATTTAGACATCTATAGAACATATAT 5512
DB 1021 CGAATTTCTCAATTTCTGGAGACCCATATGAGACATTTAGACATCTATAGAACATATAT 1080

QY	5513	GTAATGTATATTAAACGTACTTAAGTCGAATTTTATGACCAAGTAAATTAATATGCGG	5572
Db	1081	GTAATGTATATTAAACGTACTTAAGTCGAATTTTATGACCAAGTAAATTAATATGCGG	1140
QY	5573	AATGTACATGCTAAATATCGAGTTTAAACTATTTTTCCAATATACAACTATTTCTCTT	5632
Db	1141	AATGTACATGCTAAATATCGAGTTTAAACTATTTTTCCAATATACAACTATTTCTCTT	1200
QY	5633	TCGTCCAACTTATATACCTTATCTGATTTCTTATTTTCTTCTTTTAAATTCCTTTTCC	5692
Db	1201	TCGTCCAACTTATATACCTTATCTGATTTCTTATTTTCTTCTTTTAAATTCCTTTTCC	1260
QY	5693	TTTCCCAAGACAAATAAATAATATACAGAAACGAAATAAGAGATTTTAAATAATCA	5752
Db	1261	TTTCCCAAGACAAATAAATAATATACAGAAACGAAATAAGAGATTTTAAATAATCA	1320
QY	5753	TAAACCCAGAGAAATATGACCTAAATTCAGACTAATCCCCCAAAATTTTCAGAAATTTATG	5812
Db	1321	TAAACCCAGAGAAATATGACCTAAATTCAGACTAATCCCCCAAAATTTTCAGAAATTTATG	1380
QY	5813	TATTTTTCGGAATTAATATTTGTTTCAAAATCAATATATGCGCCAACTAACTAATTTGAAAGA	5872
Db	1381	TATTTTTCGGAATTAATATTTGTTTCAAAATCAATATATGCGCCAACTAACTAATTTGAAAGA	1440
QY	5873	CAATGGAATGACTGAAACCATCATATCTCTCAAGTCTCAACCTATGAAGAAATCATGTA	5932
Db	1441	CAATGGAATGACTGAAACCATCATATCTCTCAAGTCTCAACCTATGAAGAAATCATGTA	1500
QY	5933	ACCAATAGACTATCATGATTTAGTTAATGATGATCATATATGTTTCTTTTGAACATA	5992
Db	1501	ACCAATAGACTATCATGATTTAGTTAATGATGATCATATATGTTTCTTTTGAACATA	1560
QY	5993	GATATGTCATTTATCTGGATATAAAGATGGCGTTTTTAAACCTACTTTTGCAATTTTGTAT	6052
Db	1561	GATATGTCATTTATCTGGATATAAAGATGGCGTTTTTAAACCTACTTTTGCAATTTTGTAT	1620
QY	6053	ATCTTTCTTCTAATACATATGATCAATACACTTTTGTGTTTTTAAAGAAATTAATAACTTA	6112
Db	1621	ATCTTTCTTCTAATACATATGATCAATACACTTTTGTGTTTTTAAAGAAATTAATAACTTA	1680
QY	6113	TTTCAACATCGATCAATTTTACTTTTGTGTTTTTCCATATGACTATATAGGCTCAC	6172
Db	1681	TTTCAACATCGATCAATTTTACTTTTGTGTTTTTCCATATGACTATATAGGCTCAC	1740
QY	6173	ACTTTT 6178	
Db	1741	ACTTTT 1746	
RESULT 3			
US-10-033-190-3/c			
; Sequence 3, Application US/10033190			
; Publication No. US20020133848A1			
; GENERAL INFORMATION:			
; APPLICANT: Exelixis Plant Sciences, Inc.			
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF AN ANTHOCYANIN MUTANT (ANT			
; TITLE OF INVENTION: TOMATO			
; FILE REFERENCE: EP01-002C			
; CURRENT APPLICATION NUMBER: US/10/033,190			
; CURRENT FILING DATE: 2001-10-29			
; PRIOR APPLICATION NUMBER: US 60/244,685			
; PRIOR FILING DATE: 2000-10-30			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 3			
; LENGTH: 10078			
; TYPE: DNA			
; ORGANISM: pag3202			
US-10-033-190-3			
Query Match 18.5%; Score 1402.4; DB 5; Length 10078;			
Best Local Similarity 99.9%; Pred. No. 4.9e-245;			

Matches 1403; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	6177	TTGTTTCGGATCTAGATATACATCAATCCACTTGTCTTTGAAGACGTGGTTGGAAACGTCT	6236
Db	4251	TAGTTTCGGATCTAGATATACATCAATCCACTTGTCTTTGAAGACGTGGTTGGAAACGTCT	4192
QY	6237	TCTTTTTCACGATGTTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAG	6296
Db	4191	TCTTTTTCACGATGTTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAG	4132
QY	6297	GCATCTTGAACGATAGCCCTTTCTTTATCGCAATGATGGCAATTTGTAGAACCCATCTTCC	6356
Db	4131	GCATCTTGAACGATAGCCCTTTCTTTATCGCAATGATGGCAATTTGTAGAACCCATCTTCC	4072
QY	6357	TTTTCTACTGTCCTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCCGAGGAGGTTT	6416
Db	4071	TTTTCTACTGTCCTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCCGAGGAGGTTT	4012
QY	6417	CCCGATATTACCCCTTTGTTGAAAAGTCTCAATAGCCCTCTCGTCTTCTGAGACTGTATCT	6476
Db	4011	CCCGATATTACCCCTTTGTTGAAAAGTCTCAATAGCCCTCTCGTCTTCTGAGACTGTATCT	3952
QY	6477	TTGATATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCA	6536
Db	3951	TTGATATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCA	3892
QY	6537	CATCAATCCACTGCTTTGAAAGCGTGGTTGGAAGCTCTTCTTTTCCACGATGTTCTCTC	6596
Db	3891	CATCAATCCACTGCTTTGAAAGCGTGGTTGGAAGCTCTTCTTTTCCACGATGTTCTCTC	3832
QY	6597	GTGGGTGGGGGTCCATCTTTGGGACCACTGTCTGGTAGAGGCATCTTGAACGATAGCCCTT	6656
Db	3831	GTGGGTGGGGGTCCATCTTTGGGACCACTGTCTGGTAGAGGCATCTTGAACGATAGCCCTT	3772
QY	6657	CCTTTATCGCAATGATGGCATTTGTAGAACCATCTCTCTTTCTACTGTCCTTTTCGATG	6716
Db	3771	CCTTTATCGCAATGATGGCATTTGTAGAACCATCTCTCTTTCTACTGTCCTTTTCGATG	3712
QY	6717	AAGTGACAGATAGCTGGGCAATGGAAATCCGAGGAGTTTCCCGATATTACCTTTGTTGA	6776
Db	3711	AAGTGACAGATAGCTGGGCAATGGAAATCCGAGGAGTTTCCCGATATTACCTTTGTTGA	3652
QY	6777	AAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGAG	6836
Db	3651	AAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGAG	3592
QY	6837	AGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTTGTTGAA	6896
Db	3591	AGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTTGTTGAA	3532
QY	6897	GACGTGGTTGGAACGTCTTCTTTTCCACGATGTTCTCTGGGGGGGGTCCATCTTTTG	6956
Db	3531	GACGTGGTTGGAACGTCTTCTTTTCCACGATGTTCTCTGGGGGGGGTCCATCTTTTG	3472
QY	6957	GGACCACCTGTCTGGTAGAGGCATCTTGAACGATAGCTTTTCTTTATCGCAATGATGGCAT	7016
Db	3471	GGACCACCTGTCTGGTAGAGGCATCTTGAACGATAGCTTTTCTTTATCGCAATGATGGCAT	3412
QY	7017	TTGTAGAAAGCCATCTTCTTTTCTACTGTCTCTTTTCGATGAAGTGCAGATAGCTGGGCAA	7076
Db	3411	TTGTAGAAAGCCATCTTCTTTTCTACTGTCTCTTTTCGATGAAGTGCAGATAGCTGGGCAA	3352
QY	7077	TGGAATCCGAGGAGGTTTCCCGATATTACCTTTGTTGAAAGTCTCAATAGCCCTCTGG	7136
Db	3351	TGGAATCCGAGGAGGTTTCCCGATATTACCTTTGTTGAAAGTCTCAATAGCCCTCTGG	3292
QY	7137	TCCTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGAGAGTGTCTGTCCTCCACCATG	7196
Db	3291	TCCTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGAGAGTGTCTGTCCTCCACCATG	3232
QY	7197	TTGGGGATCTAGATATCAATCAATCCACTTGTCTTTGGAAGCGTGGTTGGAACGCTTCT	7256
Db	3231	TTGGGGATCTAGATATCAATCAATCCACTTGTCTTTGGAAGCGTGGTTGGAACGCTTCT	3172

QY 7257 TTTTCCAGATGTTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGGTAGAGCA 7316
DB 3171 TTTTCCAGATGTTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGGTAGAGCA 3112
QY 7317 TCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCCCTTT 7376
DB 3111 TCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCCCTTT 3052
QY 7377 TCTACTGCTCTTTCCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCC 7436
DB 3051 TCTACTGCTCTTTCCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCC 2992
QY 7437 GATATTACCTTTGTTGAAAAGTCTCAATAGGCCCTCTGGTCTTCTTGAGACTGTATCTTTG 7496
DB 2991 GATATTACCTTTGTTGAAAAGTCTCAATAGGCCCTCTGGTCTTCTTGAGACTGTATCTTTG 2932
QY 7497 ATATTCTTGGAGTAGACGAGAGTGTGCTCCACCATGTTGGGATCCACTAGTCTTAG 7556
DB 2931 ATATTCTTGGAGTAGACGAGAGTGTGCTCCACCATGTTGGGATCCACTAGTCTTAG 2872
QY 7557 AGCGGCCGCCACCGCGGTGGAGCT 7580
DB 2871 AGCGGCCGCCACCGCGGTGGAGCT 2848

RESULT 4

US-09-522-334-1/c

; Sequence 1, Application US/09522334

; Patent No. US20020157130A1

; GENERAL INFORMATION:

; APPLICANT: Wagner, Ry

; APPLICANT: Mathews, Helena

; APPLICANT: Liu, Xing Liang

; APPLICANT: Waggoner, Wency J.

; TITLE OF INVENTION: TRAIT-ASSOCIATED GENE IDENTIFICATION

; FILE OF INVENTION: METHOD

; FILE REFERENCE: 4257-0018.30

; CURRENT APPLICATION NUMBER: US/09/522,334

; CURRENT FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: US 60/124,232

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1361

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: modified enhancer

US-09-522-334-1

Query Match 17.9%; Score 1360; DB 3; Length 1361;

Best Local Similarity 100.0%; Pred. No. 1.1e-237; Mismatches 0; Gaps 0;

Matches 1360; Conservative 0; Indels 0

QY 6179 GTTTCGGATCTAGATATCACATCAATCCACTTGTTCGAGACGCTGGTTGGAACGCTCTTC 6238
DB 1360 GTTTCGGATCTAGATATCACATCAATCCACTTGTTCGAGACGCTGGTTGGAACGCTCTTC 1301
QY 6239 TTTTTCACGATGTTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGGTAGAGC 6298
DB 1300 TTTTTCACGATGTTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGGTAGAGC 1241
QY 6299 ATCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTT 6358
DB 1240 ATCTTGAACGATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTT 1181
QY 6359 TTCTACTGTCCTTTCTGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCC 6418
DB 1180 TTCTACTGTCCTTTCTGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCC 1121
QY 6419 CGATATTACCCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT 6478

DB 1120 CGATATTACCCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT 1061
QY 6479 GATATTCTTGGAGTAGACGAGAGTGTGCTGTCCACCATGTTGGGATCTAGATATCACA 6538
DB 1060 GATATTCTTGGAGTAGACGAGAGTGTGCTGTCCACCATGTTGGGATCTAGATATCACA 1001
QY TCAATCCACTGCTTTGGAAGAGTGGTGGAAAGTCTTCTTTTCCAGATGTTCTCTGT 6598
DB 1000 TCAATCCACTGCTTTGGAAGAGTGGTGGAAAGTCTTCTTTTCCAGATGTTCTCTGT 941
QY GGTGGGGGTCCATCTTTGGGACCACTGTGCTGAGAGGATCTTCCGATATTAACCTTTGTTGAA 6658
DB 940 GGTGGGGGTCCATCTTTGGGACCACTGTGCTGAGAGGCACTTGGAAAGTCTTCTTCC 881
QY TTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTCTACTGCTCTTTTCGATGAA 6718
DB 880 TTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTCTACTGCTCTTTTCGATGAA 821
QY GTGACAGATAGTGGGCAATGGAATCCGAGGAGGTTTCCGATATTAACCTTTGTTGAA 6778
DB 820 GTGACAGATAGTGGGCAATGGAATCCGAGGAGGTTTCCGATATTAACCTTTGTTGAA 761
QY AGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAG 6838
DB 760 AGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAG 701
QY AGTGTGCTGTCTCCACCATGTTGGGATCTAGATATCACATCAATCCACTTGTCTTGAAGA 6898
DB 700 AGTGTGCTGTCTCCACCATGTTGGGATCTAGATATCACATCAATCCACTTGTCTTGAAGA 641
QY CGTGGTTGGAACGCTCTTCTTTTCCAGATGTTCTGCTGGTGGGGGTCATCTTTGGG 6958
DB 640 CGTGGTTGGAACGCTCTTCTTTTCCAGATGTTCTGCTGGTGGGGGTCATCTTTGGG 581
QY ACCACTGTCGGTAGAGGCACTTTGAAACGATAGCCCTTCTTCTTATCGCAATGATGCAATTT 7018
DB 580 ACCACTGTCGGTAGAGGCACTTTGAAACGATAGCCCTTCTTCTTATCGCAATGATGCAATTT 521
QY GTAGAAGCCATCTTCTTCTTCTACTGTCTCTTTCGATGAAGTGACAGATAGCTGGGCAATG 7078
DB 520 GTAGAAGCCATCTTCTTCTTCTACTGTCTTTCGATGAAGTGACAGATAGCTGGGCAATG 461
QY GAATCCGAGGAGGTTTCCGATATTAACCTTTGTTGAAAAGTCTCAATAGCCCTCTGCTTC 7138
DB 460 GAATCCGAGGAGGTTTCCGATATTAACCTTTGTTGAAAAGTCTCAATAGCCCTCTGCTTC 401
QY TTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTT 7198
DB 400 TTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTT 341
QY GGGGATCTAGATATCACATCAATCCACTTGTTCGAGACGCTGGTTGGAACGCTCTTCTTT 7258
DB 340 GGGGATCTAGATATCACATCAATCCACTTGTTCGAGACGCTGGTTGGAACGCTCTTCTTT 281
QY TTCCACGATGTTCTGCTGGGTGGGGTCCATCTTTGGGACCACTGTGCTGAGAGGCAATC 7318
DB 280 TTCCACGATGTTCTGCTGGGTGGGGTCCATCTTTGGGACCACTGTGCTGAGAGGCAATC 221
QY TTGAACGATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTCTTC 7378
DB 220 TTGAACGATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTCTTC 161
QY TACTGTCTCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA 7438
DB 160 TACTGTCTCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA 101
QY TATTACCCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT 7498
DB 100 TATTACCCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT 41
QY ATTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTTG 7538

Db 40 ATTCTTGAGTAGACGAGAGTGTGCTGCTCCACCATGTTG 1

RESULT 5

US-10-650-249-17
; Sequence 17, Application US/10650249
; Publication No. US20040045055A1
; GENERAL INFORMATION:
; APPLICANT: Neff, Michael M
; TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING

; FILE REFERENCE: WSHU 2064.1
; CURRENT APPLICATION NUMBER: US/10/650,249
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,657
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1235
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

US-10-650-249-17

Query Match 16.3%; Score 1235; DB 7; Length 1235;

Best Local Similarity 100.0%; Pred. No. 6.4e-215; Mismatches 0; Indels 0; Gaps 0;
Matches 1235; Conservative 0

QY 3045 CAACCAAGAACGATGACGTATATGATGACCTTGCAAAAATAAGCAAAACAAATACCTGTT 3104

Db 1 CAACCAAGAACGATGACGTATATGATGACCTTGCAAAAATAAGCAAAACAAATACCTGTT 60

QY 3105 CAAATCGACACTTAATTCGAAAAGGTTAGTAATAGTAAGAGGCTTTTATTATGAAA 3164

Db 61 CAAATCGACACTTAATTCGAAAAGGTTAGTAATAGTAAGAGGCTTTTATTATGAAA 120

QY 3165 ACACAAAAGAAAATAAGAGCCTTAAGAGATGATGAAAATTTGAAAGAGAAAAAGAGCATTG 3224

Db 121 ACACAAAAGAAAATAAGAGCCTTAAGAGATGATGAAAATTTGAAAGAGAAAAAGAGCATTG 180

QY 3225 TTATAGAAAAGAAAATAAGAGAGAGTAAAGAGAAATTAAGAAACAACAATAAATTAACA 3284

Db 181 TTATAGAAAAGAAAATAAGAGAGAGTAAAGAGAAATTAAGAAACAACAATAAATTAACA 240

QY 3285 AGGAAACTTCATTTCTCTTTATCCATTCAGCTCCTCCCTCTCTCTCTCTCTCTCTCTCT 3344

Db 241 AGGAAACTTCATTTCTCTTTATCCATTCAGCTCCTCCCTCTCTCTCTCTCTCTCTCTCT 300

QY 3345 CTCCTCTCTCTAGATCAATTCCTTCTATGATGATGATATCCACCATATCTCGACC 3404

Db 301 CTCCTCTCTCTAGATCAATTCCTTCTATGATGATGATATCCACCATATCTCGACC 360

QY 3405 TCTTACCTAAAGGATACAAGTAAAGATTCAAAAGATGGTTTTCTCATCTCTTCCAGTG 3464

Db 361 TCTTACCTAAAGGATACAAGTAAAGATTCAAAAGATGGTTTTCTCATCTCTTCCAGTG 420

QY 3465 AATCAGTTCGATTCACAAAATGGGACGAGGTAAATAACAGTTTATGATATTTGCTAGAT 3524

Db 421 AATCAGTTCGATTCACAAAATGGGACGAGGTAAATAACAGTTTATGATATTTGCTAGAT 480

QY 3525 GTTTCCTGATTCGTTCTTTCTCCAGCTCGATCAAGATTTATGAAAATTTGATGAGA 3584

Db 481 GTTTCCTGATTCGTTCTTTCTCCAGCTCGATCAAGATTTATGAAAATTTGATGAGA 540

QY 3585 TTTTGTTCGACAAAATTCCTAGCTATTTGTGACGCGCATATATATTACTTATGAATATTC 3644

Db 541 TTTTGTTCGACAAAATTCCTAGCTATTTGTGACGCGCATATATATTACTTATGAATATTC 600

QY 3645 TTAGTTGATTAACCCCTTTTTTTCTCTCTCGAATATACGAAAATATATAAAGAT 3704

Db 601 TTAGTTGATTAACCCCTTTTTTTCTCTCTCGAATATACGAAAATATATAAAGAT 660

QY 3705 GATTTCAATTTTGGTCTTTTCTTCTACCTTCAAGACTTTTAAAAAATATTCTTAGTTGA 3764

Db 661 GATTTCAATTTTGGTCTTTTCTTCTCAAGACTTTTAAAAAATATTCTTAGTTGA 720

QY 3765 TAAAAACCTTTTCTTCTCTCAAGGCTTATGATATATGATGTTTTCTTACAGGATT 3824

Db 721 TAAAAACCTTTTCTTCTCTCAAGGCTTATGATATATGATGTTTTCTTACAGGATT 780

QY 3825 AATTTTCTCTTTGGTTAGATTTTACACCGCATCGAATATTCACCTCAAAAAATAAAAA 3884

Db 781 AATTTTCTCTTTGGTTAGATTTTACACCGCATCGAATATTCACCTCAAAAAATAAAAA 840

QY 3885 GTTTAAAGTTACTATGACTTTAACTGAGTTATTTATCCATTTCTTTTGCAGCTTTGT 3944

Db 841 GTTTAAAGTTACTATGACTTTAACTGAGTTATTTATCCATTTCTTTTGCAGCTTTGT 900

QY 3945 TGA AAAAATAAATTAATCTGCAATCTTGTCAAAGTAGTCACAATTTTATCTATTTTC 4004

Db 901 TGA AAAAATAAATTAATCTGCAATCTTGTCAAAGTAGTCACAATTTTATCTATTTTC 960

QY 4005 TTTTGTCTCCGACCAATGTTTCAAACTCGAATCTTTCTGTTAAAAAGTTGTTTCTGCTTTA 4064

Db 961 TTTTGTCTCCGACCAATGTTTCAAACTCGAATCTTTCTGTTAAAAAGTTGTTTCTGCTTTA 1020

QY 4065 TTATAAACCTCAAACTAATTAAGTACAAATTAATGTTAATATGCAAGGGAACCAACATC 4124

Db 1021 TTATAAACCTCAAACTAATTAAGTACAAATTAATGTTAATATGCAAGGGAACCAACATC 1080

QY 4125 AGCTAGATGTTGTCACAATCTGCAAGACCTTAATTAATTAATCTTACGGCAGCTCTCATCAC 4184

Db 1081 AGCTAGATGTTGTCACAATCTGCAAGACCTTAATTAATTAATCTTACGGCAGCTCTCATCAC 1140

QY 4185 CACGACCTTCAGGTTGCGAGTTCGAGTCAAGCTAGAGTGAATTCATGTTGGAACGTG 4244

Db 1141 CACGACCTTCAGGTTGCGAGTTCGAGTCAAGCTAGAGTGAATTCATGTTGGAACGTG 1200

QY 4245 CTCGGATCGCAAAAGTCCCATTTGCTGGAAGCAGCT 4279

Db 1201 CTCGGATCGCAAAAGTCCCATTTGCTGGAAGCAGCT 1235

RESULT 6

US-10-650-249-20
; Sequence 20, Application US/10650249
; Publication No. US20040045055A1
; GENERAL INFORMATION:
; APPLICANT: Neff, Michael M
; TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING

; FILE REFERENCE: WSHU 2064.1
; CURRENT APPLICATION NUMBER: US/10/650,249
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,657
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

US-10-650-249-20

Query Match 14.0%; Score 1062; DB 7; Length 1062;

Best Local Similarity 100.0%; Pred. No. 2.1e-183; Mismatches 0; Indels 0; Gaps 0;
Matches 1062; Conservative 0

QY 5117 TAAGTACTCAGCAGCTAGCTATTTCTTGATGATTTCTTTGTTGGTGGGTGACATGGTG 5176

Db 1 TAAGTACTCAGCAGCTAGCTATTTCTTGATGATTTCTTTGTTGGTGGGTGACATGGTG 60

QY 5177 CTTGTGATCGAGTTTATTTGCTGAGGAAGATCAAAACCATGAGCTATATCCAAAGGCTAAT 5236

Db 61 CTTGTGATCGAGTTTATTTGCTGAGGAAGATCAAAACCATGAGCTATATCCAAAGGCTAAT 120

```
QY 5237 TTTGAGGCTCAAGGAAGGTATGGTTATATAAATCTATCTTTTGTGATCTTTTAAAGATCT 5296
Db 121 TTTGAGGCTCAAGGAAGGTATGGTTATATAAATCTATCTTTTGTGATCTTTTAAAGATCT 180
QY 5297 TCAAAAGTGTAGTATGTTTATTTGGTTGGCTTCTGGTGATATTTATGTTTATTTAGAAATTT 5356
Db 181 TCAAAAGTGTAGTATGTTTATTTGGTTGGCTTCTGGTGATATTTATGTTTATTTAGAAATTT 240
QY 5357 GGTCTTATATATTTGGCTATATATAGAGGTGTGGGTGATATGTATGAATTCAGAGTTGAT 5416
Db 241 GGTCTTATATATTTGGCTATATATAGAGGTGTGGGTGATATGTATGAATTCAGAGTTGAT 300
QY 5417 GTTGGAACTTTTGTGTGTTTCATTGAATATCATCGAATCTCAATTTCTTGGAGACC 5476
Db 301 GTTGGAACTTTTGTGTGTTTCATTGAATATCATCGAATCTCAATTTCTTGGAGACC 360
QY 5477 CATTATGAGACATTTGAGACATCTATAGAACATATATGTAATGTAATTTAAACGCTACTTAA 5536
Db 361 CATTATGAGACATTTGAGACATCTATAGAACATATATGTAATGTAATTTAAACGCTACTTAA 420
QY 5537 GTCGAATTTTATGACCAAGTAATAATTAATGCGGAATGACATGCTTAATATCGAGTTT 5596
Db 421 GTCGAATTTTATGACCAAGTAATAATTAATGCGGAATGACATGCTTAATATCGAGTTT 480
QY 5597 AAACATATTTTCCATATATCAACTATTTTCTCTTTCGTCGAATCTATATCTTAT 5656
Db 481 AAACATATTTTCCATATATCAACTATTTTCTCTTTCGTCGAATCTATATCTTAT 540
QY 5657 CTGATTTCTTATTTCTTTTAAATCTTTTCTTTTCCAGACACAAAAA 5716
Db 541 CTGATTTCTTATTTCTTTTAAATCTTTTCTTTTCCAGACACAAAAA 600
QY 5717 AATCAGAAACGAAAAAGAGATTTTAAAAATTCATAACCCAGAGAAATTTATGCACCTA 5776
Db 601 AATCAGAAACGAAAAAGAGATTTTAAAAATTCATAACCCAGAGAAATTTATGCACCTA 660
QY 5777 AATTCAGACTAATCCCCAAATTTTCAAGAAATTTATGTAATTTTGGGATTTAATTTGT 5836
Db 661 AATTCAGACTAATCCCCAAATTTTCAAGAAATTTATGTAATTTTGGGATTTAATTTGT 720
QY 5837 TCAGAACTAATGCGCAACTAATCTAATTTGAAAGACAAATGGAATGACTGAAACCATGCA 5896
Db 721 TCAGAACTAATGCGCAACTAATCTAATTTGAAAGACAAATGGAATGACTGAAACCATGCA 780
QY 5897 TAACTCTCAAGTCTCAACCTATGAAGAAATCATGTAAACCAATAGACTATCATGATTA 5956
Db 781 TAACTCTCAAGTCTCAACCTATGAAGAAATCATGTAAACCAATAGACTATCATGATTA 840
QY 5957 GTTAATGCATGATCTATATGTAATTTCTTTGAACATAGATATGTCATTTATCTGGATATA 6016
Db 841 GTTAATGCATGATCTATATGTAATTTCTTTGAACATAGATATGTCATTTATCTGGATATA 900
QY 6017 AGATGGGCTTTAACTACTTTGCAATTTTGTATATCTTTCTTAATACATATGATC 6076
Db 901 AGATGGGCTTTAACTACTTTGCAATTTTGTATATCTTTCTTAATACATATGATC 960
QY 6077 AATACACTTTTGTTTTAAAGAAATTTAAACCTTATTTTCAACATCATCATTTTAA 6136
Db 961 AATACACTTTTGTTTTAAAGAAATTTAAACCTTATTTTCAACATCATCATTTTAA 1020
QY 6137 CTTTGTGTTCCATATATGACTACATTTATAGGCTCACATTTT 6178
Db 1021 CTTTGTGTTCCATATATGACTACATTTATAGGCTCACATTTT 1062
```

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RESULT 7
US-10-650-249-19
; Sequence 19, Application US/10650249
; Publication No. US2004004055A1
; GENERAL INFORMATION:
; APPLICANT: Neff, Michael M
; TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
; TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
```

```
; FILE REFERENCE: WSHU 2064.1
; CURRENT APPLICATION NUMBER: US/10/650,249
; PRIOR FILING DATE: 2003-08-28
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1058
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-19
```

```
Query Match 14.0%; Score 1058; DB 7; Length 1058;
Best Local Similarity 100.0%; Pred. No. 1.2e-182;
Matches 1058; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3045 CAACCAAGAACGATGACGTATATGATTTGACCTTGCAAAAAATAGCAAAACAAATACCTGTT 3104
Db 1 CAACCAAGAACGATGACGTATATGATTTGACCTTGCAAAAAATAGCAAAACAAATACCTGTT 60
QY 3105 CAAATCGACACTTAATTCCAAAAAAGGTTAGTAATAGTAAGTAAGGCTTTTATATGAAA 3164
Db 61 CAAATCGACACTTAATTCCAAAAAAGGTTAGTAATAGTAAGTAAGGCTTTTATATGAAA 120
QY 3165 ACAAAGAAATAAAGAGCCTTAAGAGATGATGAAATTTGAAGAGAAAAAGAGCATTTG 3224
Db 121 ACAAAGAAATAAAGAGCCTTAAGAGATGATGAAATTTGAAGAGAAAAAGAGCATTTG 180
QY 3225 TTATAGAAAAAGAAAAAGAGAGAGTAAGAGAAATTAAGAAAAACAATAAATAAACA 3284
Db 181 TTATAGAAAAAGAAAAAGAGAGAGTAAGAGAAATTAAGAAAAACAATAAATAAACA 240
QY 3285 AGGAACTTCAATTTCTTCTTTATCCCAATTCAGCTCTCTCTCTCTCTCTCTCTCTCT 3344
Db 241 AGGAACTTCAATTTCTTCTTTATCCCAATTCAGCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 3345 CTCTCTCTCTAGATCAATTTCTTCTTTATGATGATGATTTATCCACATATCTCGGACC 3404
Db 301 CTCTCTCTCTAGATCAATTTCTTCTTTATGATGATGATTTATCCACATATCTCGGACC 360
QY 3405 TCTTACCTTAAAGAGATACAAAGATTAAGAGATTTCAAAGATGGTTTCTCATCTCTCCAGTG 3464
Db 361 TCTTACCTTAAAGAGATACAAAGATTAAGAGATTTCAAAGATGGTTTCTCATCTCTCAGTG 420
QY 3465 AATCAGTTCCGATTTCCCAAAATTTGGCAGCAGGTAAAAATCAGTTTATGATATTTGCTAGAT 3524
Db 421 AATCAGTTCCGATTTCCCAAAATTTGGCAGCAGGTAAAAATCAGTTTATGATATTTGCTAGAT 480
QY 3525 GTTTCGATTCGTTCTCTTTTCTTCCAAAGCTCGATCAAGATTTATGAAAAATTTGATGAGA 3584
Db 481 GTTTCGATTCGTTCTCTTTTCTTCCAAAGCTCGATCAAGATTTATGAAAAATTTGATGAGA 540
QY 3585 TTTTGTTCGACAAATTTCTTAGCTATTTGTGACGCGCATATATATTACTTTATGAATATTC 3644
Db 541 TTTTGTTCGACAAATTTCTTAGCTATTTGTGACGCGCATATATATTACTTTATGAATATTC 600
QY 3645 TTAGTTGATTAACCCCTTTTCTTCTCTTCTCGAATATACGAAATATATATAAGAT 3704
Db 601 TTAGTTGATTAACCCCTTTTCTTCTCTTCTCGAATATACGAAATATATATAAGAT 660
QY 3705 GATTTCAAATTTGGCTTTTCTTCTTCTCAAGACTTTTAAAAAATTTATTTCTTAGTGGA 3764
Db 661 GATTTCAAATTTGGCTTTTCTTCTTCTCAAGACTTTTAAAAAATTTATTTCTTAGTGGA 720
QY 3765 TAAAAACCTTTTCTTCTTCTTCTTCCAGGCTTATGTAATGTTTCTTACAGGATTT 3824
Db 721 TAAAAACCTTTTCTTCTTCTTCTTCCAGGCTTATGTAATGTTTCTTACAGGATTT 780
QY 3825 AATTTCTCTTTGGTTAGATTTTACACCGCATGGAATTTACTCTTCAAAAAATAAAAA 3884
Db 781 AATTTCTCTTTGGTTAGATTTTACACCGCATGGAATTTACTCTTCAAAAAATAAAAA 840
```


Qy 4652 GGAACCTCAAAATAGCAACATGATAGTGGTATGAGTCTTAGTGGTGGGATCTTGGATGCA 4711
Db 421 GGAACCTCAAAATAGCAACATGATAGTGGTATGAGTCTTAGTGGTGGGATCTTGGATGCA 480
Qy 4712 TGGAGATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACAACACTACCGGA 4771
Db 481 TGGAGATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACAACACTACCGGA 540
Qy 4772 TTGGTGCATCTTCAAAACGCTTATATCCATTTACTAGAGGTAAAGGAGGTGTTAATCAA 4831
Db 541 TTGGTGCATCTTCAAAACGCTTATATCCATTTACTAGA----- 578
Qy 4832 GGTGATCTCAACAGAGAGTAGTGATTTATTCCTCAATCAGCTAAATGTTTAAAGCCCTTGATG 4891
Db 579 ----- 578
Qy 4892 GATTTTCTTCAGCGGGGTTAGCGCCACGCAAAATGTGAAGCGGGAAGAGAAAT 4951
Db 579 -----AGCGGGGTTAGCGCCACGCAAAATGTGAAGCGGGAAGAGAAAT 627
Qy 4952 GATCAGGATCGGGTAGGGATGGGATGGAGTGAATTAATTTATCAAGAACTTTTGGGT 5011
Db 628 GATCAGGATCGGGTAGGGATGGGATGGAGTGAATTAATTTATCAAGAACTTTTGGGT 687
Qy 5012 AATATCAACATAAACTCAGGAGGAAACGAGGAATACACATCATGCGGAGGTAAACAGTTCT 5071
Db 688 AATATCAACATAAACTCAGGAGGAAACGAGGAATACACATCATGCGGAGGTAAACAGTTCT 747
Qy 5072 TGGACCGGTTTCACTCCAACTCAACAGGCCATCTCTCATTTCTAA 5119
Db 748 TGGACCGGTTTCACTCCAACTCAACAGGCCATCTCTCATTTCTAA 795

RESULT 11

US-10-225-066A-409
; Sequence 409, Application US/10225066A
; Publication No. US20050160493A9
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROWN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MB10036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 409
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-409

Query Match 9.1%; Score 692; DB 9; Length 795;
Best Local Similarity 89.5%; Pred. No. 5.7e-116;
Matches 795; Conservative 0; Mismatches 0; Indels 93; Gaps 1;
Qy 4232 ATGTTGGAACGTTGCTCGGATCGCAAAAGTCCCATTTGCTGGAAGCAGCTCTAAATTTGCCCT 4291
Db 1 ATGTTGGAACGTTGCTCGGATCGCAAAAGTCCCATTTGCTGGAAGCAGCTCTAAATTTGCCCT 60
Qy 4292 AGATGTGACTCAACCAATATCTAAGTTCTGTGTACTTCAATAACTATAGCCTTACTCAACCT 4351
Db 61 AGATGTGACTCAACCAATATCTAAGTTCTGTGTACTTCAATAACTATAGCCTTACTCAACCT 120
Qy 4352 CGCCATTTCTGCAAAAACATGTCGCTATTGGACACGTCGCGGTCTCTTGAAGAAATGTT 4411
Db 121 CGCCATTTCTGCAAAAACATGTCGCTATTGGACACGTCGCGGTCTCTTGAAGAAATGTT 180
Qy 4412 CCTGTTGAGAGAGGCTTTAGGAGGAACAAGAGAGCAAAATCCAGATCGAAATCTACGGTC 4471
Db 181 CCTGTTGAGAGAGGCTTTAGGAGGAACAAGAGAGCAAAATCCAGATCGAAATCTACGGTC 240
Qy 4472 GTGGTCTCGACTGATATATCTAGTACTTTCATCCTTACTTCTCGCCCAAGTTACTCA 4531
Db 241 GTGGTCTCGACTGATATATCTAGTACTTTCATCCTTACTTCTCGCCCAAGTTACTCA 300
Qy 4532 AACCTTAGCAAGTTTTCATAGCTACGGTCAAAATCCCGAGTTTAAATTCCAAATTCGCCATC 4591
Db 301 AACCTTAGCAAGTTTTCATAGCTACGGTCAAAATCCCGAGTTTAAATTCCAAATTCGCCATC 360
Qy 4592 TTGCTCTCTCCAAAGCCTTGGAGATTACAATTTCAAGCAACACTGGATTAGATTGCT 4651
Db 361 TTGCTCTCTCCAAAGCCTTGGAGATTACAATTTCAAGCAACACTGGATTAGATTGCT 420
Qy 4652 GGAACCTCAAAATAGCAACATGATAGTGGTATGAGTCTTAGTGGGATCTTGGATGCA 4711
Db 421 GGAACCTCAAAATAGCAACATGATAGTGGTATGAGTCTTAGTGGGATCTTGGATGCA 480
Qy 4712 TGGAGATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACAACACTACCGGA 4771
Db 481 TGGAGATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACAACACTACCGGA 540
Qy 4772 TTGGTGCATCTTCAAAACGCTTATATCCATTTACTAGAGGTAAAGGAGGTGTTAATCAA 4831
Db 541 TTGGTGCATCTTCAAAACGCTTATATCCATTTACTAGA----- 578
Qy 4832 GGTGATCTCAACAGAGAGTAGTGATTTTCCCAATCAGCTAAATGTTTAAAGCCCTTGATG 4891
Db 579 ----- 578
Qy 4892 GATTTTCTTCAGCGGGGTTAGCGCCACGCAAAATGTGAAGCGGGAAGAGAAAT 4951
Db 579 -----AGCGGGGTTAGCGCCACGCAAAATGTGAAGCGGGAAGAGAAAT 627
Qy 4952 GATCAGGATCGGGTAGGGATGGGATGGAGTGAATTAATTTCTTGAAGAACTTTTGGGT 5011
Db 628 GATCAGGATCGGGTAGGGATGGGATGGAGTGAATTAATTTCTTGAAGAACTTTTGGGT 687
Qy 5012 AATATCAACATAAACTCAGGAGGAAACGAGGAATACACATCATGCGGAGGTAAACAGTTCT 5071
Db 688 AATATCAACATAAACTCAGGAGGAAACGAGGAATACACATCATGCGGAGGTAAACAGTTCT 747
Qy 5072 TGGACCGGTTTCACTCCAACTCAACAGGCCATCTCTCATTTCTAA 5119
Db 748 TGGACCGGTTTCACTCCAACTCAACAGGCCATCTCTCATTTCTAA 795

RESULT 12

US-10-650-249-15
; Sequence 15, Application US/10650249
; Publication No. US20040045055A1
; GENERAL INFORMATION:
; APPLICANT: Neff, Michael M
; TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
; ; TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT

FILE REFERENCE: WSHU 2064.1
CURRENT APPLICATION NUMBER: US/10/650,249
PRIOR FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US 60/406,657
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 684
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-10-650-249-15

Query Match 9.0%; Score 684; DB 7; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4436 AACAGAGAACCAATCCAGATCGAAATCTACGGTCGGTCTCGACTGATAATACTACT 4495
DB 1 AACAGAGAACCAATCCAGATCGAAATCTACGGTCGGTCTCGACTGATAATACTACT 60

QY 4496 AGTACTTCACTTACTTCTCGCCCAAGTTACTCAAAACCCCTAGCAAGTTTCATAGCTAC 4555
DB 61 AGTACTTCACTTACTTCTCGCCCAAGTTACTCAAAACCCCTAGCAAGTTTCATAGCTAC 120

QY 4556 GGTCAAAATCCCGAGTTTAATTCCAACTTGCCATCTTGCCCTCTCTCCAAAGCCCTTGA 4615
DB 121 GGTCAAAATCCCGAGTTTAATTCCAACTTGCCATCTTGCCCTCTCTCCAAAGCCCTTGA 180

QY 4616 GATTACAATCAAGCAACACTGGATAGATTTTGGTGGAACTCAAAATAGCAACATGATA 4675
DB 181 GATTACAATCAAGCAACACTGGATAGATTTTGGTGGAACTCAAAATAGCAACATGATA 240

QY 4676 AGTGATATGAGTTCTAGTGGGATCTTGGATGATGGAATACCTCCATCAACAA 4735
DB 241 AGTGATATGAGTTCTAGTGGGATCTTGGATGATGGAATACCTCCATCAACAA 300

QY 4736 GCTCAGCAATCCCTTTCTTGATCAACACTACCGGATTTGGTGAATCTTCAAAACCGGTTA 4795
DB 301 GCTCAGCAATCCCTTTCTTGATCAACACTACCGGATTTGGTGAATCTTCAAAACCGGTTA 360

QY 4796 TATCATTACTAGAGTTAAGGAGTGTAACTCAAGTGATTTCTCAACAGAGTAGT 4855
DB 361 TATCATTACTAGAGTTAAGGAGTGTAACTCAAGTGATTTCTCAACAGAGTAGT 420

QY 4856 GATTATTCGAATCAGCTAATGTTTAAGCCCTTGATGGATTTTCTCAGCGGGGTAGC 4915
DB 421 GATTATTCGAATCAGCTAATGTTTAAGCCCTTGATGGATTTTCTCAGCGGGGTAGC 480

QY 4916 GCCACGCAACCAAGAAATGTGAAGCGGAAGAGAAATGATCAGGATCGGGGTAGGATGG 4975
DB 481 GCCACGCAACCAAGAAATGTGAAGCGGAAGAGAAATGATCAGGATCGGGGTAGGATGG 540

QY 4976 GATGAGTGAATAACTTATCAAGAACTTTTGGGTATATCAACATAACTCAGGAGG 5035
DB 541 GATGAGTGAATAACTTATCAAGAACTTTTGGGTATATCAACATAACTCAGGAGG 600

QY 5036 AACGAGGAATACACATATGCGGAGTAACTAGTTCTTGACCGGTTTCACTCCAAACAC 5095
DB 601 AACGAGGAATACACATATGCGGAGTAACTAGTTCTTGACCGGTTTCACTCCAAACAC 660

QY 5096 TCAACAGGCCATCTCTCAATCTAA 5119
DB 661 TCAACAGGCCATCTCTCAATCTAA 684

RESULT 13
US-10-161-403-90
Sequence 90, Application US/10161403
Publication No. US20030119104A1
GENERAL INFORMATION:
APPLICANT: Perkins, Edward
APPLICANT: Perez, Carl

APPLICANT: Lindenbaum, Michael
APPLICANT: Greene, Amy
APPLICANT: Leung, Josephine
APPLICANT: Fleming, Elena
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 90
LENGTH: 8428
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pCambia3300 Plasmid
US-10-161-403-90

Query Match 8.1%; Score 617.2; DB 6; Length 8428;
Best Local Similarity 93.6%; Pred. No. 7.3e-103;
Matches 659; Conservative 0; Mismatches 33; Indels 12; Gaps 1;

QY 6868 AGATATACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 6927
DB 7146 AGATATACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 7205

QY 6928 TGTCTCTCGTGGTGGGGTCCATCTTTGGGACCACTCTCGGTAGAGGATCTTGAACGA 6987
DB 7206 TGTCTCTCGTGGTGGGGTCCATCTTTGGGACCACTCTCGGTAGAGGATCTTGAACGA 7265

QY 6988 TAGCCTTCTCTTATCGCAATGATGGCATTTGTAGAACCCATCTCTTTTCTACTGTCC 7047
DB 7266 TAGCCTTCTCTTATCGCAATGATGGCATTTGTAGGTGCCACCTCTCTTTTCTACTGTCC 7325

QY 7048 TTTCGATGAAGTGACAGATAGCTGGGCAATCGAATCCGAGGAGTTTCCCGATATTACCC 7107
DB 7326 TTTTGTGAAAGTGACAGATAGCTGGGCAATCGAATCCGAGGAGTTTCCCGATATTACCC 7385

QY 7108 TTTGTGAAAGTGCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTGG 7167
DB 7386 TTTGTGAAAGTGCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTGG 7445

QY 7168 AGTAGACGAGAGTGTCTGTCTCCACCATGTTGGGGATCTAGATATCATCATCAATCACTT 7227
DB 7446 AGTAGACGAGAGTGTCTGTCTCCACCATGTTGGGGATCTAGATATCATCATCAATCACTT 7493

QY 7228 GCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGATGTTCTCGTGGGTGGGGTC 7287
DB 7494 GCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGATGTTCTCGTGGGTGGGGTC 7553

QY 7288 CATCTTTGGGACCACTGTCTGGTAGAGGCAATCTTGAACGATAGCCCTTCTTTTATCGCAAT 7347
DB 7554 CATCTTTGGGACCACTGTCTGGTAGAGGCAATCTTGAACGATAGCCCTTCTTTTATCGCAAT 7613

QY 7348 GATGCAATTTGTAGAACCCATCTTCTCTTCTACTGTCTTCTGATGAGTACAGATAG 7407
DB 7614 GATGCAATTTGTAGAACCCATCTTCTCTTCTACTGTCTTCTGATGAGTACAGATAG 7673

QY 7408 CTGGCAATGAATCCGAGGAGGTTTCCCGATATTACCTTTTGTGAAAAGTCTCAATAG 7467
DB 7674 CTGGCAATGAATCCGAGGAGGTTTCCCGATATTACCTTTTGTGAAAAGTCTCAATAG 7733

QY 7468 CCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTCTCGTCT 7527
DB 7734 CCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTCTCGTCT 7793

QY 7528 CCACCATGTTGGGATTCACCTAGTCTTAGAGGGCCGCCACCGC 7571

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Db 7794 CCACCATGTTGGCAAGCTGCTCTAGCCCAATACGCAAAACCGCCTC 7837
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US-10-161-408-2
; Sequence 2, Application US/10161408
; Publication No. US20040214290A1
; GENERAL INFORMATION:
; APPLICANT: Perez, Carl
; APPLICANT: Fabijanski, Steven
; APPLICANT: Perkins, Edward
; TITLE OF INVENTION: Plant Artificial Chromosomes, Uses thereof, and Methods of Preparing
; TITLE OF INVENTION: Plant Artificial Chromosomes
; FILE REFERENCE: 24601-419
; CURRENT APPLICATION NUMBER: US/10/161,408
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/294,687
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/296,329
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 8428
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pCambia3300 plasmid
US-10-161-408-2

Query Match 8.1%; Score 617.2; DB 8; Length 8428;
Best Local Similarity 93.6%; Pred. No. 7.3e-102;
Matches 659; Conservative 0; Mismatches 33; Indels 12; Gaps 1;

QY 6868 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 6927
|||||
Db 7146 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 7205
|||||
QY 6928 TGTCTCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGCATCTTTGAAACGA 6987
|||||
Db 7206 TGCTCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGCAGAGGCATCTTTGAAACGA 7265
|||||
QY 6988 TAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAACCATCTCTCTTTCTACTGTCC 7047
|||||
Db 7266 TAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAACCATCTCTCTTTCTACTGTCC 7325
|||||
QY 7048 TTTGATGAAGTACAGATAGTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 7107
|||||
Db 7326 TTTGATGAAGTACAGATAGTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 7385
|||||
QY 7108 TTTGTTGAAAAGTCTCAATAGCCCTCTCGTCTTCTGAGACTGTATCTTTGATATTCTTGG 7167
|||||
Db 7386 TTTGTTGAAAAGTCTCAATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTCTTGG 7445
|||||
QY 7168 AGTAGACAGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCAATCAATCCACTT 7227
|||||
Db 7446 AGTAGACAGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCAATCAATCCACTT 7493
|||||
QY 7228 GCTTTGAAAGCTGTTGGAACGCTCTCTTTTCCACGATGTTCTCGTGGGTGGGGTTC 7287
|||||
Db 7494 GCTTTGAAAGCTGTTGGAACGCTCTCTTTTCCACGATGTTCTCGTGGGTGGGGTTC 7553
|||||
QY 7288 CATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAAACGATAGCCCTTTCTTTATCGCAAT 7347
|||||
Db 7554 CATCTTTGGGACCACTGTCGGCAGAGGCATCTTGAAACGATAGCCCTTTCTTTATCGCAAT 7613
|||||
QY 7348 GATGCAATTTGTAGAAGCCATCTCTTTTCTACTGTCTTTTCGATGAGTGACAGATAG 7407
|||||
Db 7614 GATGCAATTTGTAGAAGCCATCTCTTTTCTACTGTCTTTTTCGATGAGTGACAGATAG 7673
|||||
QY 7408 CTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCCTTTGTTGAAAAGTCTCAATAG 7467
|||||
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Db 7674 CTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCCTTTGTTGAAAAGTCTCAATAG 7733
|||||
QY 7468 CCCTCTGCTCTTCTGAGACTGTATCTTTGATATTCTTTGAGTAGACGAGAGTGTCTGCT 7527
|||||
Db 7734 CCCTTTGGTCTTCTGAGACTGTATCTTTGATATTCTTTGAGTAGACGAGAGTGTCTGCT 7793
|||||
QY 7528 CCACCATGTTGGGATCCACTAGTTCTTAGAGCGCCGCCACCCG 7571
|||||
Db 7794 CCACCATGTTGGCAAGCTGCTCTAGCCCAATACGCAAAACCGCCTC 7837
|||||

RESULT 15
US-11-006-076-90
; Sequence 90, Application US/11006076
; Publication No. US20050181506A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 17084-02202/420B
; CURRENT APPLICATION NUMBER: US/11/006,076
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 8428
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pCambia3300 Plasmid
US-11-006-076-90

Query Match 8.1%; Score 617.2; DB 10; Length 8428;
Best Local Similarity 93.6%; Pred. No. 7.3e-102;
Matches 659; Conservative 0; Mismatches 33; Indels 12; Gaps 1;

QY 6868 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 6927
|||||
Db 7146 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 7205
|||||
QY 6928 TGTCTCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGCATCTTTGAAACGA 6987
|||||
Db 7206 TGCTCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGCAGAGGCATCTTTGAAACGA 7265
|||||
QY 6988 TAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAACCATCTCTCTTTCTACTGTCC 7047
|||||
Db 7266 TAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAACCATCTCTCTTTCTACTGTCC 7325
|||||
QY 7048 TTTGATGAAGTACAGATAGTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 7107
|||||
Db 7326 TTTGATGAAGTACAGATAGTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 7385
|||||
QY 7108 TTTGTTGAAAAGTCTCAATAGCCCTCTCGTCTTCTGAGACTGTATCTTTGATATTCTTGG 7167
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Db 7386 TTTGTTGAAAAGTCTCAATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTCTTGG 7445
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QY 7168 AGTAGACAGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCAATCAATCCACTT 7227
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Db 7446 AGTAGACAGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCAATCAATCCACTT 7493
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QY 7228 GCTTTGAAAGCTGTTGGAACGCTCTCTTTTCCACGATGTTCTCGTGGGTGGGGTTC 7287
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Db 7494 GCTTTGAAAGCTGTTGGAACGCTCTCTTTTCCACGATGTTCTCGTGGGTGGGGTTC 7553
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QY 7288 CATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAAACGATAGCCCTTTCTTTATCGCAAT 7347
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Db 7554 CATCTTTGGGACCACTGTCGGCAGAGGCATCTTGAAACGATAGCCCTTTCTTTATCGCAAT 7613
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QY 7348 GATGCAATTTGTAGAAGCCATCTCTTTTCTACTGTCTTTTCGATGAGTGACAGATAG 7407
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Db 7614 GATGCAATTTGTAGAAGCCATCTCTTTTCTACTGTCTTTTTCGATGAGTGACAGATAG 7673
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QY 7408 CTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCCTTTGTTGAAAAGTCTCAATAG 7467
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Db	7554	CATCTTTGGGACCACTGTCGGCAGAGGCATCTTGAAACGATAGCCCTTTCCTTTATCGCAAT	7613
Qy	7348	GATGGCATTTGTAGAAAGCATCTTCCTTTTCTACTGTCCTTTTCGATGAAGTGACAGATAG	7407
Db	7614	GATGGCATTTGTAGAGTGCACCTTCCTTTTCTACTGTCCTTTTGATGAAGTGACAGATAG	7673
Qy	7408	CTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCCTTTGTTGAAAAGTCTCAATAG	7467
Db	7674	CTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCCTTTGTTGAAAAGTCTCAATAG	7733
Qy	7468	CCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTGTCCT	7527
Db	7734	CCCTTTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTGTCCT	7793
Qy	7528	CCACCATGTTGGGATCCACTAGTTCTAGAGGGCCGCCCGC	7571
Db	7794	CCACCATGTTGGCAAGTGTCTTAGCCAATACGCAACCGCCTC	7837

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Job time : 3577 secs

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OM nucleic - nucleic search, using sw model

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Perfect score: 7580
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB ID	Description
	Score	Match Length		
C 1	621	8.2	5033	US-08-038-768A-1
C 2	617.2	8.1	12614	Sequence 1, Appli
C 3	563	7.4	2728	Sequence 1, Appli
C 4	554.2	7.3	1138	Sequence 7, Appli
C 5	554.2	7.3	1138	Sequence 8, Appli
C 6	462.2	6.1	907	Sequence 9, Appli
C 7	461	6.1	14446	Sequence 17, Appli
C 8	461	6.1	14446	Sequence 3, Appli
C 9	379.8	5.0	1800	Sequence 4, Appli
C 10	379.8	5.0	1800	Sequence 29, Appli
C 11	379.8	5.0	1800	Sequence 29, Appli
C 12	379.8	5.0	1800	Sequence 29, Appli
C 13	379.2	5.0	1742	Sequence 30, Appli
C 14	379.2	5.0	1742	Sequence 30, Appli
C 15	379.2	5.0	1742	Sequence 30, Appli
C 16	379.2	5.0	1742	Sequence 30, Appli
C 17	377.6	5.0	661	Sequence 33, Appli
C 18	377.6	5.0	661	Sequence 33, Appli
C 19	377.6	5.0	2107	Sequence 29, Appli
C 20	377.6	5.0	2122	Sequence 25, Appli
C 21	377.6	5.0	2436	Sequence 31, Appli
C 22	377.6	5.0	3469	Sequence 23, Appli
C 23	377.6	5.0	3469	Sequence 23, Appli
C 24	377.6	5.0	3754	Sequence 15, Appli

C 25	377.6	5.0	3754	US-10-232-665-15	Sequence 15, Appli
C 26	377.6	5.0	8012	US-09-182-117-1	Sequence 1, Appli
C 27	377.6	5.0	8012	US-09-434-039A-1	Sequence 1, Appli
C 28	377.6	5.0	8349	US-09-186-002-16	Sequence 16, Appli
C 29	377.6	5.0	8418	US-09-182-117-5	Sequence 5, Appli
C 30	377.6	5.0	8418	US-09-434-039A-5	Sequence 5, Appli
C 31	377.6	5.0	8798	US-09-182-117-4	Sequence 4, Appli
C 32	377.6	5.0	8798	US-09-434-039A-4	Sequence 4, Appli
C 33	377.6	5.0	10249	US-09-186-002-14	Sequence 14, Appli
C 34	377.6	5.0	10339	US-09-186-002-13	Sequence 13, Appli
C 35	374.6	4.9	1030	US-07-936-163-46	Sequence 46, Appli
C 36	374.6	4.9	1030	US-08-729-601A-43	Sequence 43, Appli
C 37	374.6	4.9	1196	US-08-729-601A-46	Sequence 46, Appli
C 38	374.6	4.9	5897	US-09-097-319A-26	Sequence 26, Appli
C 39	374.6	4.9	5897	US-09-643-971-26	Sequence 26, Appli
C 40	374.6	4.9	9335	US-09-097-319A-19	Sequence 19, Appli
C 41	374.6	4.9	9335	US-09-643-971-19	Sequence 19, Appli
C 42	374.6	4.9	10160	US-09-097-319A-8	Sequence 8, Appli
C 43	374.6	4.9	10160	US-09-643-971-8	Sequence 8, Appli
C 44	374.6	4.9	11784	US-09-097-319A-9	Sequence 9, Appli
C 45	374.6	4.9	11784	US-09-643-971-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-038-768A-1/c
; Sequence 1. Application US/08038768A
; Patent No. 5569828
; GENERAL INFORMATION:
; APPLICANT: McMullen, Michael D.; Roth, Bradley A.; Townsend,
; APPLICANT: Rod
; TITLE OF INVENTION: MAIZE CHLOROTIC DWARF VIRUS RESISTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust
; STREET: Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; OPERATING SYSTEM: MS-DOS, Microsoft Windows
; SOFTWARE: Microsoft Windows No. 5569828epad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,768A
; FILING DATE: 19930324
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Roth, Michael J.
; REGISTRATION NUMBER: 29,342
; REFERENCE/DOCKET NUMBER: 0235 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 245-3594
; TELEFAX: (515) 245-3634
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5033 base pairs
; TYPE: nucleotide
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: synthetic DNA
; DESCRIPTION: transformation plasmid pPH11406
; HYPOTHETICAL: NO
US-08-038-768A-1

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Query Match      8.2%; Score 621; DB 2; Length 5033;
Best Local Similarity 95.1%; Pred. No. 2.8e-111;
Matches 653; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

QY 6868 AGATATACATCAATCCACTTCTTTGAAGACGTGGTGGAAACGTCCTTTTCCACGA 6927
Db 1103 AGATATACATCAATCCACTTCTTTGAAGACGTGGTGGAAACGTCCTTTTCCACGA 1044
QY 6928 TGTTCCTCGTGGGTGGGTCCATCTTTGGGACCACTGTCGTAGAGGATCTTGAACGA 6987
Db 1043 TGCTCCTCGTGGGTGGGTCCATCTTTGGGACCACTGTCGTAGAGGATCTTGAACGA 984
QY 6988 TAGCCTTTCTTTATCGCAATGATGCGATTTCTGGAAGCCTCTCTTTCTACTGTCC 7047
Db 983 TAGCCTTTCTTTATCGCAATGATGCGATTTCTGGAAGCCTCTCTTTCTACTGTCC 924
QY 7048 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 7107
Db 923 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 864
QY 7108 TTTTGTGAAAAGTCTCAATAGACCTCTGCTCTCTGAGACTGTATCTTTGATATCTTGG 7167
Db 863 TTTTGTGAAAAGTCTCAATAGACCTTTGGTCTCTGAGACTGTATCTTTGATATCTTGG 804
QY 7168 AGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCTCT---AGATATCAATCAATCC 7223
Db 803 AGTAGACGAGAGTGTCTGCTCCACCATGTTGACGATTTCTAGAGCATCAATCAATCC 744
QY 7224 ACTTGTGTTGAAGACGTGGTGGAAACGTCCTTTTCCACGATGTTCTCGTGGGTGGG 7283
Db 743 ACTTGTGTTGAAGACGTGGTGGAAACGTCCTTTTCCACGATGTTCTCGTGGGTGGG 684
QY 7284 GGTCCATCTTTGGGACCACTGTCGTAGAGGATCTTGAACATAGCCTTTCTTTATCG 7343
Db 683 GGTCCATCTTTGGGACCACTGTCGTAGAGGATCTTGAACATAGCCTTTCTTTATCG 624
QY 7344 CAATGATGCAATTTGTAGAAGCCTCTCTCTTTCTACTGTCTCTTGCATGAAGTGACAG 7403
Db 623 CAATGATGCAATTTGTAGTGCCACTCTCTTTCTACTGTCTCTTGCATGAAGTGACAG 564
QY 7404 ATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCTTTGTTGAAAAGTCTCA 7463
Db 563 ATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCTTTGTTGAAAAGTCTCA 504
QY 7464 ATAGCCCTCGTCTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAGTGCG 7523
Db 503 ATAGCCCTTTGGTCTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAGTGCG 444
QY 7524 TGCTCCACCATGTTGGGATCCCACTAG 7550
Db 443 TGCTCCACCATGTTGACGATTTCTAG 417
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RESULT 2
US-09-577-424-1/c
; Sequence 1, Application US/09577424
; Patent No. 6525245
; GENERAL INFORMATION:
; APPLICANT: Rhoads, David M
; TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
; TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS
; FILE REFERENCE: UNL2990
; CURRENT APPLICATION NUMBER: US/09/577,424
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 12614
; TYPE: DNA
; ORGANISM: Bacterial Plasmid DNA - Plasmid pZP-ALE
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1665)..(3317)
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US-09-577-424-1
Query Match      8.1%; Score 617.2; DB 3; Length 12614;
Best Local Similarity 93.6%; Pred. No. 1.9e-110;
Matches 659; Conservative 0; Mismatches 33; Indels 12; Gaps 1;

QY 6868 AGATATACATCAATCCACTTCTTTGAAGACGTGGTGGAAACGTCCTTTTCCACGA 6927
Db 4915 AGATATACATCAATCCACTTCTTTGAAGACGTGGTGGAAACGTCCTTTTCCACGA 4856
QY 6928 TGTTCCTCGTGGGTGGGTCCATCTTTGGGACCACTGTCGTAGAGGATCTTGAACGA 6987
Db 4855 TGCTCCTCGTGGGTGGGTCCATCTTTGGGACCACTGTCGTAGAGGATCTTGAACGA 4796
QY 6988 TAGCCTTTCTTTATCGCAATGATGCGATTTCTGGAAGCCTCTCTTTCTACTGTCC 7047
Db 4795 TAGCCTTTCTTTATCGCAATGATGCGATTTCTGGAAGCCTCTCTTTCTACTGTCC 4736
QY 7048 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 7107
Db 4735 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 4676
QY 7108 TTTTGTGAAAAGTCTCAATAGACCTCTGCTCTCTGAGACTGTATCTTTGATATCTTGG 7167
Db 4675 TTTTGTGAAAAGTCTCAATAGACCTTTGGTCTCTGAGACTGTATCTTTGATATCTTGG 4616
QY 7168 AGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCTTAGATATCAATCAATCACTT 7227
Db 4615 AGTAGACGAGAGTGTCTGCTCCACCATGT-----TATCAATCAATCACTT 4568
QY 7228 GCTTTGAAGACGTGGTGGAAACGTCCTTTTCCACGATGTTCTCGTGGGTGGGTGTC 7287
Db 4567 GCTTTGAAGACGTGGTGGAAACGTCCTTTTCCACGATGTCCTCGTGGGTGGGTGTC 4508
QY 7288 CATCTTTGGGACCACTGTCGTAGAGGATCTTGAACATAGCCTTTCTTTATCGCAAT 7347
Db 4507 CATCTTTGGGACCACTGTCGTAGAGGATCTTGAACATAGCCTTTCTTTATCGCAAT 4448
QY 7348 GATGCAATTTGTAGAAGCCTCTCTCTTTCTACTGTCTCTTGCATGAAGTACAGATAG 7407
Db 4447 GATGCAATTTGTAGTGCCACTCTCTTTCTACTGTCTCTTTGATGAAGTACAGATAG 4388
QY 7408 CTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCTTTGTTGAAAAGTCTCAATAG 7467
Db 4387 CTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCTTTGTTGAAAAGTCTCAATAG 4328
QY 7468 CCCTCTGTCTTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAGTGTCGTCT 7527
Db 4327 CCCTTTGGTCTTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAGTGTCGTCT 4268
QY 7528 CCACCATGTTGGGATCCCACTAGTTCTAGAGCGCGCCACCGC 7571
Db 4267 CCACCATGTTGGCAAGCTGCTCTAGCCAAATAGCGAAACCGCCTC 4224
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RESULT 3
US-08-836-402B-7/c
; Sequence 7, Application US/08836402B
; Patent No. 6063988
; GENERAL INFORMATION:
; APPLICANT: Rudiger Hain, Regina Fischer
; TITLE OF INVENTION: DNA SEQUENCE AND ITS USE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG KRAMER SCHAEFER & BRISCOE
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Gateway 2000
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; OPERATING SYSTEM: DOS
; SOFTWARE: Microsoft Windows 98
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,402B
; FILING DATE: 02-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 44 40 200.7 (Germany)
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 9840-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2728 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-08-836-402B-7

Query Match 7.4%; Score 563; DB 3; Length 2728;
Best Local Similarity 97.7%; Pred. No. 4.6e-100;
Matches 607; Conservative 0; Mismatches 0; Indels 14; Gaps 3;

QY 6190 AGATATCACATCAATCCACTCTGTTGAAGACGTCGTTGGAAACGTCCTCTTTTCCACGA 6249
DB 627 AGATATCACATCAATCCACTCTGTTGAAGACGTCGTTGGAAACGTCCTCTTTTCCACGA 568
QY 6250 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGAGAGGCA-TCTTGAACG 5308
DB 567 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGAGAGGCAATCTTGAACG 508
QY 6309 ATAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTC 6368
DB 507 ATAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTC 448
QY 6369 CTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACC 6428
DB 447 CTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACC 388
QY 6429 CTTTGTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTG 6488
DB 387 CTTTGTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTG 328
QY 6489 GAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGATCTAGATATCACATCAATCCACT 6548
DB 327 GAGTAGACGAGAGTGTCGTGCTCCACCATGT-----TATCATCAATCCACT 280
QY 6549 TGTCTTTGAAGACGTCGTTGGAAACGTCCTTTTCCACGATGTTCTCGTGGGTGGGGT 6608
DB 279 TGTCTTTGAAGACGTCGTTGGAAACGTCCTTTTCCACGATGTTCTCGTGGGTGGGGT 220
QY 6609 CCATCTTTGGGACCACTGTCGAGTAGAGGCA-TCTTGAAGCATAGGCTTCTTTATCGCA 6667
DB 219 CCATCTTTGGGACCACTGTCGAGTAGAGGCAATCTTGAACGATAGGCTTCTTTATCGCA 160
QY 6668 ATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTCCTTTTCGATGAAGTGACAGAT 6727
DB 159 ATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTCCTTTTCGATGAAGTGACAGAT 100
QY 6728 AGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCCTTTGTGAAAAGTCTCAAT 6787
DB 99 AGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCCTTTGTGAAAAGTCTCAAT 40
QY 6788 AGCCCTCTGGTCTTCTGAGAC 6808
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DB 39 AGCCCTCTGGTCTTCTGAGAC 19
RESULT 4
US-09-011-151-8/c
; Sequence 8, Application US/09011151
; Patent No. 6380463
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; FILE REFERENCE: PPD 50059/UST
; CURRENT APPLICATION NUMBER: US/09/011,151
; CURRENT FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: PCT/GB96/01893
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: GB 9515941.4
; PRIOR FILING DATE: 1995-08-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Plasmid pMJB1
; US-09-011-151-8

Query Match 7.3%; Score 554.2; DB 3; Length 1138;
Best Local Similarity 92.3%; Pred. No. 1.9e-98;
Matches 621; Conservative 0; Mismatches 38; Indels 14; Gaps 3;

QY 6190 AGATATCACATCAATCCACTGTTGAAGACGTCGTTGGAAACGTCCTTCTTTCCACG 6248
DB 681 AGATATCACATCAATCCACTGTTGAAGACGTCGTTGGAAACGTCCTTCTTTCCACG 622
QY 6249 ATGTTCTCGTGGGTGGGGTCCATCTTTGGACCACTGTCGAGAGGCAATCTTGAACG 6308
DB 621 ATGTTCTCGTGGGTGGGGTCCATCTTTGGACCACTGTCGAGAGGCAATCTTGAACG 562
QY 6309 ATAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTC 6368
DB 561 ATAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTCCACTATC 502
QY 6369 CTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACC 6428
DB 501 TTCACATAAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACC 442
QY 6429 CTTTGTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTG 6488
DB 441 CTTTGTGAAAAGTCTCAATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTCTTG 382
QY 6489 GAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGATCTAGATATCACATCAATCCACT 6548
DB 381 GAGTAGACGAGAGTGTCGTGCTCCACCATGT-----TATCATCAATCCACT 334
QY 6549 TGTCTTTGAAGACGTCGTTGGAAACGTCCTTTTCCACGATGTTCTCGTGGGTGGGGT 6607
DB 333 TGTCTTTGAAGACGTCGTTGGAAACGTCCTTTTCCACGATGTCCTCTCGTGGGTGGGGT 274
QY 6608 TCCATCTTTGGGACCACTGTCGAGTAGAGGCAATCTTGAAGCATAGGCTTCTTTATCGCA 6667
DB 273 TCCATCTTTGGGACCACTGTCGAGTAGAGGCAATCTTGAAGCATAGGCTTCTTTATCGCA 214
QY 6668 ATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTCCTTTTCGATGAAGTGACAGAT 6727
DB 213 ATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTCCTTTTCGATGAAGTGACAGAT 154
QY 6728 AGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCCTTTGTGAAAAGTCTCAAT 6787
DB 153 AGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCCTTTGTGAAAAGTCTCAAT 94
QY 6788 AGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTCTGCTG 6847
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Db 93 TGCCTTTGGTCTTCTGAGACTGTATCTTTGATATTTTGGAGTAGACAAGTGTGCTGTG 34

Qy 6848 CTCACCATGTTG 6860
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Db 33 CTCACCATGTTG 21

RESULT 5
US-09-011-151-9
; Sequence 9, Application US/09011151
; Patent No. 6380463
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; TITLE OF INVENTION: DNA Constructs
; FILE REFERENCE: PPD 50059/UST
; CURRENT APPLICATION NUMBER: US/09/011,151
; CURRENT FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: PCT/GB96/01883
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: GB 9515941.4
; PRIOR FILING DATE: 1995-08-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Plasmid pMJBI
US-09-011-151-9

Query Match 7.3%; Score 554.2; DB 3; Length 1138;
Best Local Similarity 92.3%; Pred. No. 1.9e-98;
Matches 621; Conservative 0; Mismatches 38; Indels 14; Gaps 3;

Qy 6190 AGATATCATCAATCCACTTGTCTTTGAGAGCTGGTTGGACGCTTTC-TTTTCCACG 6248

Db 458 AGATATCATCAATCCACTTGTCTTTGAGAGCTGGTTGGACGCTTTC-TTTTCCACG 517

Qy 6249 ATGTTCTCGTGGGTGGGTCATCTTTGGACCACTGTCCGTAGAGGCATCTTGAACG 6308

Db 518 ATGCTCTCGTGGGTGGGTCATCTTTGGACCACTGTCCGTAGAGGCATCTTCAACG 577

Qy 6309 ATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAGCCATCTTCTTTCTACTGTC 6368

Db 578 ATGGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAGCCATCTTCTTTCCACTATC 637

Qy 6369 CTTTCGATGAAGTGACAGTAGCTGGCAATCGAATCCGAGAGGTTTCCCGATATTACC 6428

Db 638 TTCACAATAAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACC 697

Qy 6429 CTTTGTGTAAGAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATATTCTTG 6488

Db 698 CTTTGTGTAAGAGTCTCAATAGCCCTTGGTCTTCTGAGACTGTATCTTTGATATTCTTG 757

Qy 6489 GAGTAGACGAGAGTGTGCTGCCATCTTGGGATCTAGATATCAATCAATCCACT 6548

Db 758 GAGTAGACAGAGTGTGCTGCCATCTTGGGATCTAGATATCAATCAATCCACT 805

Qy 6549 TGCCTTTGAAGAGCTGGTTGGACGCTTTC-TTTTCCAGATGTTCCCTGCTGGGTGGGG 6607

Db 806 TGCCTTTGAAGAGCTGGTTGGACGCTTTC-TTTTCCAGATGTTCCCTGCTGGGTGGGG 865

Qy 6608 TCCATCTTTGGGACCACTGTCCGTAGAGGCATCTTGAACGATAGCCCTTCTTTATTCGCA 6667

Db 866 TCACTTTTGGGACCACTGTCCGAGAGGCATCTTCAAGATGGCCCTTCTTTATTCGCA 925

Qy 6668 ATGATGGCAATTTGTAGAGCCATCTTCTTTTCTACTGCTCTTTGATGAAGTGACAGAT 6727

Db 926 ATGATGGCAATTTGTAGAGCCATCTTCTTTTCTACTGCTCTTTGATGAAGTGACAGAT 985

Qy 6728 AGCTGGCAATGGAATCCGAGAGGTTTCCCGATATTACCCTTTGTTGAAAGTCTCAAT 6787
|||||

Db 986 AGCTGGCAATGGAATCCGAGAGGTTTCCGGATATTACCCTTTGTGAAAGTCTCAAT 1045

Qy 6788 AGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAGTGTGCTG 6847
|||||

Db 1046 TGCCTTTTGGTCTTCTGAGACTGTATCTTTGATATTTTGGAGTAGACAAGTGTGCTG 1105
|||||

Qy 6848 CTCACCATGTTG 6860
|||||

Db 1106 CTCACCATGTTG 1118

RESULT 6
US-09-623-551-17/c
; Sequence 17, Application US/09623551
; Patent No. 6774281
; GENERAL INFORMATION:
; APPLICANT: Stuiver, Maarten
; APPLICANT: Custers, Jerome
; APPLICANT: Simons, Lambertus
; TITLE OF INVENTION: Method For The Induction Of Pathogen Resistance In
; TITLE OF INVENTION: Plants
; FILE REFERENCE: MOG57706/UST
; CURRENT APPLICATION NUMBER: US/09/623,551
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: EP 98104076.9
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: PCT/EP99/01672
; PRIOR FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Combination of
; OTHER INFORMATION: 35S Promoter with the Glucanase II leader
US-09-623-551-17

Query Match 6.1%; Score 462.2; DB 3; Length 907;
Best Local Similarity 80.4%; Pred. No. 1.4e-80;
Matches 602; Conservative 0; Mismatches 43; Indels 104; Gaps 1;

Qy 6190 AGATATCATCAATCCACTTGTCTTTGAGAGCTGGTTGGACGCTTCTTTTCCACGA 6249

Db 766 AGATATCATCAATCCACTTGTCTTTGAGAGCTGGTTGGACGCTTCTTTTCCACGA 707

Qy 6250 TGTTCCTCGTGGGTGGGTCATCTTTGGGACCACTGTCCGTAGAGGCATCTTCAACGA 6309

Db 706 TGTTCCTCGTGGGTGGGTCATCTTTGGGACCACTGTCCGTAGAGGCATCTTCAACGA 647

Qy 6310 TAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAACCATCTTCTTTCTACTGTCC 6369

Db 646 TGGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAGGCATCTTCTTTCTACTGTCT 587

Qy 6370 TTTCCATGAAGTGACAGATAGCTGGCAATCGAATCCGAGAGGTTTCCCGATATTACC 6429

Db 586 TCACAATAAAGTGACAGATAGCTGGCAATCGAATCCGAGAGGTTTCCCGATATTACC 527

Qy 6430 TTTTGTGTAAGAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATATTCTTG 6489

Db 526 TTTTGTGTAAGAGTCTCAATAGCCCTTGGTCTTCTGAGACTGTATCTTTGATATTCTTG 467

Qy 6490 AGTAGACGAGAGTGTGCTGCCATCTTCCCATGTTGGGA----- 6525

Db 466 AGTAGACAGAGTGTGCTGCCATCTTCCCATGTTGGGA----- 407

Qy 6526 ----- 6525

Db 406 GTAAGAGACTCTGTATGAACCTGTTCCCGAGTCTTTACGGCGAGTCTGTAGGTCTCTTA 347

Qy 6526 -----TCTAGATATCAATCAATCCACTTGTCTTTGAAAGCTGTGTT 6565
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Db 346 TTGAAATCTTTGACTCCATCGGAATTATCAATCAATCCACTTGTCTTTGAAGACGTGT 287
QY 6566 TGAACGCTCTCTTTTCCAGATGTTCTCGTGGGTGGGGTCCATCTTTGGGACCACT 6625
Db 286 TGAACGCTCTCTTTTCCAGATGTTCTCGTGGGTGGGGTCCATCTTTGGGACCACT 227
QY 6626 GTGCGTAGAGGATCTTGAACATAGCCCTTCTCTTATCGCAATGATGCGCATTTGTAGAA 6685
Db 226 GTGCGCAGAGGATCTTCAACATAGCCCTTCTCTTATCGCAATGATGCGCATTTGTAGAA 167
QY 6686 GCATCTCTCTTTCTACTGTCTCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCC 6745
Db 166 GCACCTCTCTTTTCCATATCTTCAATATGAAGTGACAGATAGCTGGGCAATGGAATCC 107
QY 6746 GAGGAGTTTCCGATATACCTTTTGTGTTGAAAGTCTCAATAGCCCTCTGCTCTCTGA 6805
Db 106 GAGGAGTTTCCGATATACCTTTTGTGTTGAAAGTCTCAATAGCCCTTTGCTCTCTGA 47
QY 6806 GACTGTATCTTTGATATCTTTGGAGTAGA 6834
Db 46 GACTGTATCTTTGATATCTTTGGAGTAGA 18

RESULT 7
US-09-810-861B-3/c
; Sequence 3, Application US/09810861B
; Patent No. 6770799
; GENERAL INFORMATION:
; APPLICANT: Mor, Tsafir S.
; APPLICANT: Soreq, Hermona
; APPLICANT: Arntzen, Charles J.
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
; TITLE OF INVENTION: TRANSGENIC PLANTS
; FILE REFERENCE: BTI-45
; CURRENT APPLICATION NUMBER: US/09/810,861B
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,440
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3
; TYPE: DNA
; LENGTH: 5767
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid vector
; OTHER INFORMATION: pTM034.
US-09-810-861B-3

Query Match 6.1%; Score 461; DB 3; Length 5767;
Best Local Similarity 86.5%; Pred. No. 3.9e-80;
Matches 582; Conservative 0; Mismatches 0; Indels 91; Gaps 3;
QY 6190 AGATATCACATCAATCCACTTGTGTAAGACGTGTGGAAACGCTCTCTTTTCCACGA 6249
Db 603 AGATATCACATCAATCCACTTGTGTAAGACGTGTGGAAACGCTCTCTTTTCCACGA 544
QY 6250 TGTCTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCA-TCCTGAACG 6308
Db 543 TGTCTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCAATCTTGAACG 484
QY 6309 ATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCTACTGTC 6368
Db 483 ATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCTACTGTC 424
QY 6369 CTTTTCGATGAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACC 6428
Db 423 CTTTTCGATGAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACC 364
QY 6429 CTTTGTGAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATATCTTTG 6488
Db 363 CTTTGTGAAAGT----- 350
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QY 6489 GAGTAGACGAGAGTGTGTGCTCCACCATGTTGGGATCTAGATATCAATCAATCCACT 6548
Db 349 -----TATCATCAATCCACT 333
QY 6549 TGCTTTGAAGACGTGTTGGAACGCTCTCTTTTCCAGATGTTCTCTCGTGGGTGGGGT 6608
Db 332 TGCTTTGAAGACGTGTTGGAACGCTCTCTTTTCCAGATGTTCTCTCGTGGGTGGGGT 273
QY 6609 CCATCTTTGGGACCACTGTGCGTAGAGGCA-TCCTTGAACGATAGCCTTTCTTTATCGCA 6667
Db 272 CCATCTTTGGGACCACTGTGCGTAGAGGCAATCTTGAACGATAGCCTTTCTTTATCGCA 213
QY 6668 ATGATGGCAATTTGTAGAAGCCATCTCTTTTCTACTGTCTTTTGAAGAGTGACAGAT 6727
Db 212 ATGATGGCAATTTGTAGAAGCCATCTCTTTTCTACTGTCTTTTGAAGAGTGACAGAT 153
QY 6728 AGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCCCTTTGTTGAAAAGTCTCAAT 6787
Db 152 AGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCCCTTTGTTGAAAAGTCTCAAT 93
QY 6788 AGCCCTCTGCTCTCTGAGACTGTATCTTTGATATCTTTGGAGTAGACGAGAGTGTCTG 6847
Db 92 AGCCCTCTGCTCTCTGAGACTGTATCTTTGATATCTTTGGAGTAGACGAGAGTGTCTG 33
QY 6848 CTCACCATGTTG 6860
Db 32 CTCACCATGTTG 20
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RESULT 8

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US-09-810-861B-4/c
; Sequence 4, Application US/09810861B
; Patent No. 6770799
; GENERAL INFORMATION:
; APPLICANT: Mor, Tsafir S.
; APPLICANT: Soreq, Hermona
; APPLICANT: Arntzen, Charles J.
; APPLICANT: Mason, Hugh S.
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
; TITLE OF INVENTION: TRANSGENIC PLANTS
; FILE REFERENCE: BTI-45
; CURRENT APPLICATION NUMBER: US/09/810,861B
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,440
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4
; LENGTH: 14446
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11862)..(12157)
; OTHER INFORMATION: Description of Artificial Sequence: plasmid vector
; OTHER INFORMATION: pTM036. Identity of sequence residues 11862-12157 unknown.
US-09-810-861B-4
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Query Match 6.1%; Score 461; DB 3; Length 14446;
Best Local Similarity 86.5%; Pred. No. 5e-80;
Matches 582; Conservative 0; Mismatches 0; Indels 91; Gaps 3;
QY 6190 AGATATCACATCAATCCACTTGTGTAAGACGTGTGGAAACGCTCTCTTTTCCACGA 6249
Db 14353 AGATATCACATCAATCCACTTGTGTAAGACGTGTGGAAACGCTCTCTTTTCCACGA 14294
QY 6250 TGTCTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCA-TCCTGAACG 6308
Db 14293 TGTCTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCAATCTTTGAACG 14234
QY 6309 ATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCTACTGTC 6368
Db -----TATCATCAATCCACT 333
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Db	14233	ATAGCCTTTCCCTTATCGCAATGATGGCAATTTGTAGAGCCATCTTCTCTTCTACTGTC	14174
Qy	6369	CTTTTCGATCAAGTGACAGATAGCTCGGCAATGGAATCCGAGAGGTTTCCCGATATTACC	6428
Db	14173	CTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACC	14114
Qy	6429	CTTTGTTGAAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATCTTG	6488
Db	14113	CTTTGTTGAAAAAGT-----	14100
Qy	6489	GAGTAGACGAGAGTGTCTGGTCTCCACCATGTTGGGGATCTAGATATCAATCAATCCACT	6548
Db	14099	-----TATCAGATCAATCCACT	14083
Qy	6549	TGCTTTGAAGACGTGGTTGGAAAGCTCTTTTTCACAGATCTTCTCGTGGGTGGGGT	6608
Db	14082	TGCTTTGAAGACGTGGTTGGAAAGCTCTTCTTTTCCAGCATGTTCTCGTGGGTGGGGT	14023
Qy	6609	CCATCTTTGGGACCACTGTCGGTAGAGGCA-TCCTTGAACGATAGCTTTTCTTTATCGCA	6667
Db	14022	CCATCTTTGGGACCACTGTCGGTAGAGGCACTTTGAAAGATAGCTTTCTTTATCGCA	13963
Qy	6668	ATGATGGCAATTTGTAGAGCCATCTTCTTTTCTACTGTCCTTCGATGAAGTGACAGAT	6727
Db	13962	ATGATGGCAATTTGTAGAGCCATCTTCTTTTCTACTGTCCTTCGATGAAGTGACAGAT	13903
Qy	6728	AGCTGGGCAATGGAATCCGAGAGGTTCCCGATATTACCTTTCTTGAAGTCTCAAT	6787
Db	13902	AGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCTTTCTTGAAGTCTCAAT	13843
Qy	6788	AGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAGAGTGTCTGTG	6847
Db	13842	AGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAGAGTGTCTGTG	13783
Qy	6848	CTCCACCATGTTG 6860	
Db	13782	CTCCACCATGTTG 13770	
RESULT 9			
US-09-737-698B-29/c			
; Sequence 29, Application US/09737698B			
; Patent No. 6462258			
; GENERAL INFORMATION:			
; APPLICANT: Finchler, Karen			
; TITLE OF INVENTION: No. 6462258el Plant Expression Constructs			
; FILE REFERENCE: 38-21(51499)C			
; CURRENT APPLICATION NUMBER: US/09/737,698B			
; CURRENT FILING DATE: 2000-12-15			
; PRIOR APPLICATION NUMBER: US 60/171,173			
; PRIOR FILING DATE: 1999-12-16			
; NUMBER OF SEQ ID NOS: 30			
; SOFTWARE: Patent in version 3.0			
; SEQ ID NO 29			
; LENGTH: 1800			
; TYPE: DNA			
; ORGANISM: artificial sequence			
; FEATURE:			
; NAME/KEY: promoter			
; LOCATION: (1)..(1800)			
; OTHER INFORMATION: y = t/u or c			
; OTHER INFORMATION: chimeric promoter fusion CamV and Act8 polynucleotides + Act8 in			
; OTHER INFORMATION: tro			
US-09-737-698B-29			
Query Match			
Best Local Similarity 5.0%; Score 379.8; DB 3; Length 1800;			
Matches 489; Conservative 0; Mismatches 37; Indels 77; Gaps 1;			
Qy	6522	GGGATCTAGATATCAATCAATCCACTTCTTTGAAAGAGCTGTGGAAAGCTTCTTTT	6581
Db	535	GGAAAGCTTCTAGATATCAATCAATCCACTTCTTTGAAAGAGCTGTGGAAAGCTTCTTTT	476

Qy	6582	TCCACGATGTTCTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTTCGGTAGAGGCATCT	6641
Db	475	TCCACGATGTTCTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTTCGGTAGAGGCATCT	416
Qy	6642	TGAACGATAGCTTCTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCT	6701
Db	415	TCAACGATGGCTTCTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCT	356
Qy	6702	ACTGTCTTTTCGATCAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGAT	6761
Db	355	ACTATCTTTCAATAAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGAT	296
Qy	6762	ATTACCTTTTGTAAAAAGTCTCAATAGCCCTCTGGTCTTCTTGAGACTGTATCTTTTGATA	6821
Db	295	ATTACCTTTTGTAAAAAGTCTCA	272
Qy	6822	TTCTTGGAGTAGACGAGAGTGTCTGGTCTCCACCATGTTGGGATCTAGATATCAATCAA	6881
Db	271	-----CATCGGACCATCAATCAA	253
Qy	6882	TCCACTTCTTTGAAGACGTGGTTGGAAAGCTTCTTTTCCACGATGTCTCTCGTGGT	6941
Db	252	TCCACTTCTTTGAAGACGTGGTTGGAAAGCTTCTTTTCCACGATGTCTCTCGTGGT	193
Qy	6942	GGGGTCCCATCTTTGGGACCACTGTCTGGTAGAGGCATCTTGAACGATAGCCCTTCTTTTA	7001
Db	192	GGGGTCCCATCTTTGGGACCACTGTCTGGTAGAGGCATCTTGAACGATAGCCCTTCTTTTA	133
Qy	7002	TGCGAATGATGGCAATTTAGAACCATCTTCTTTTCTACTGTCTTTCGATGAAGTGA	7061
Db	132	TGCGAATGATGGCAATTTAGAACCATCTTCTTTTCTACTGTCTTTCGATGAAGTGA	73
Qy	7062	CAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCTTTTGTGAAAGTC	7121
Db	72	CAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCTTTTGTGAAAGTC	13
Qy	7122	TCA 7124	
Db	12	TCA 10	
RESULT 10			
US-09-737-626A-29/c			
; Sequence 29, Application US/09737626A			
; Patent No. 6660911			
; GENERAL INFORMATION:			
; APPLICANT: Finchler, Karen			
; APPLICANT: Flaszinski, Stanislaw			
; APPLICANT: Wilkinson, Jack			
; TITLE OF INVENTION: No. 6660911el Plant Expression Constructs			
; FILE REFERENCE: 38-21(51499)B			
; CURRENT APPLICATION NUMBER: US/09/737,626A			
; CURRENT FILING DATE: 2002-02-25			
; PRIOR APPLICATION NUMBER: 09/737,626			
; PRIOR FILING DATE: 2000-12-15			
; NUMBER OF SEQ ID NOS: 30			
; SOFTWARE: Patent in version 3.0			
; SEQ ID NO 29			
; LENGTH: 1800			
; TYPE: DNA			
; ORGANISM: artificial sequence			
; FEATURE:			
; NAME/KEY: promoter			
; LOCATION: (1)..(1800)			
; OTHER INFORMATION: y = t/u or c			
; OTHER INFORMATION: chimeric promoter fusion CamV and Act8 polynucleotides + Act8 in			
; OTHER INFORMATION: tro			
US-09-737-626A-29			
Query Match			
Best Local Similarity 5.0%; Score 379.8; DB 3; Length 1800;			
Matches 489; Conservative 0; Mismatches 37; Indels 77; Gaps 1;			

QY 6522 GGGATCTAGATATCATCAATCCACTTGTCTTTGAAGACGTGGTGGAAACGTCCTCTTTT 6581
|||
Db 535 GGAAGCTTGATATCATCAATCCACTTGTCTTTGAAGACGTGGTGGAAACGTCCTCTTTT 476
|||
QY 6582 TCCAGATGTTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTCTCGGTAGAGGCATCT 6641
|||
Db 475 TCCAGATGCTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTCTCGGTAGAGGCATCT 416
|||
QY 6642 TGAACGATAGCCCTTCTTTATCGCAATGATGGCAATTTGTAGAACCCATCTTCTTTTCT 6701
|||
Db 415 TCAACGATGGCCCTTCTTTATCGCAATGATGGCAATTTGTAGAACCCATCTTCTTTTCC 356
|||
QY 6702 ACTGTCCTTTGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGAT 6761
|||
Db 355 ACTATCTTCACAATAAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGAT 296
|||
QY 6762 ATTACCCCTTTGTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATA 6821
|||
Db 295 ATTACCCCTTTGTGAAAAGTCTCA----- 272
|||
QY 6822 TTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCTAGATATCATCAAA 6881
|||
Db 271 -----CATCGACCATCATCAAA 253
|||
QY 6882 TCCACTTGTCTTTGAAGACGTGGTGGAAACGTCCTTTTTCACGATGTTCTCTGGGT 6941
|||
Db 252 TCCACTTGTCTTTGAAGACGTGGTGGAAACGTCCTTTTTCACGATGTTCTCTGGGT 193
|||
QY 6942 GGGGTCCATCTTTGGGACCACTGTCTGAGGCACTCTTCTTCTACTGTCTTTCGATGAAGTGA 7061
|||
Db 132 TCGCAATGATGCAATTTGTAGAGCACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 73
|||
QY 7062 CAGATAGCTGGCAATGGAATCCGAGAGGTTTCCCGATATTTACCCCTTTGTGAAAAGTC 7121
|||
Db 72 CAGATAGCTGGCAATGGAATCCGAGAGGTTTCCCGATATTTACCCCTTTGTGAAAAGTC 13
|||
QY 7122 TCA 7124
|||
Db 12 TCA 10
|||

RESULT 11
US-10-427-169-29/c
; Sequence 29, Application US/10427169
; Patent No. 6919495
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6919495el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/427,169
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/737,626A
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1800)
; OTHER INFORMATION: y = t/u or c
; OTHER INFORMATION: chimeric promoter fusion CamV and Act8 polynucleotides + Act8 in

; OTHER INFORMATION: tto
US-10-427-169-29

Query Match 5.0%; Score 379.8; DB 3; Length 1800;
Best Local Similarity 81.1%; Pred. No. 1.8e-64;
Matches 489; Conservative 0; Mismatches 37; Indels 77; Gaps 1;

QY 6522 GGGATCTAGATATCATCAATCCACTTGTCTTTGAAGACGTGGTGGAAACGTCCTCTTTT 6581
|||
Db 535 GGAAGCTTGATATCATCAATCCACTTGTCTTTGAAGACGTGGTGGAAACGTCCTCTTTT 476
|||
QY 6582 TCCAGATGTTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTCTCGGTAGAGGCATCT 6641
|||
Db 475 TCCAGATGCTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTCTCGGTAGAGGCATCT 416
|||
QY 6642 TGAACGATAGCCCTTCTTTATCGCAATGATGGCAATTTGTAGAACCCATCTTCTTTTCT 6701
|||
Db 415 TCAACGATGGCCCTTCTTTATCGCAATGATGGCAATTTGTAGAACCCATCTTCTTTTCC 356
|||
QY 6702 ACTGTCCTTTGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGAT 6761
|||
Db 355 ACTATCTTCACAATAAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGAT 296
|||
QY 6762 ATTACCCCTTTGTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATA 6821
|||
Db 295 ATTACCCCTTTGTGAAAAGTCTCA----- 272
|||
QY 6822 TTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCTAGATATCATCAAA 6881
|||
Db 271 -----CATCGACCATCATCAAA 253
|||
QY 6882 TCCACTTGTCTTTGAAGACGTGGTGGAAACGTCCTTTTTCACGATGTTCTCTGGGT 6941
|||
Db 252 TCCACTTGTCTTTGAAGACGTGGTGGAAACGTCCTTTTTCACGATGTTCTCTGGGT 193
|||
QY 6942 GGGGTCCATCTTTGGGACCACTGTCTGAGGCACTCTTCTTCTACTGTCTTTCGATGAAGTGA 7061
|||
Db 192 GGGGTCCATCTTTGGGACCACTGTCTGAGGCACTCTTCAACGATGGCCCTTCTCTTTA 133
|||
QY 7002 TCGCAATGATGCAATTTGTAGAGCACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 73
|||
Db 132 TCGCAATGATGCAATTTGTAGAGCACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 73
|||
QY 7062 CAGATAGCTGGCAATGGAATCCGAGAGGTTTCCCGATATTTACCCCTTTGTGAAAAGTC 7121
|||
Db 72 CAGATAGCTGGCAATGGAATCCGAGAGGTTTCCCGATATTTACCCCTTTGTGAAAAGTC 13
|||
QY 7122 TCA 7124
|||
Db 12 TCA 10
|||

RESULT 12
US-10-427-180-29/c
; Sequence 29, Application US/10427180
; Patent No. 6949696
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6949696el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/427,180
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/737,626A
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 1800
; TYPE: DNA

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; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1800)
; OTHER INFORMATION: y = t/u or c
; OTHER INFORMATION: chimeric promoter fusion CamV and Act8 polynucleotides + Act8 in
; OTHER INFORMATION: tro
US-10-427-180-29

Query Match      5.0%; Score 379.8; DB 3; Length 1800;
Best Local Similarity 81.1%; Pred. No. 1.8e-64;
Matches 489; Conservative 0; Mismatches 37; Indels 77; Gaps 1;

Qy 6522 GGGATCTAGATATCACATCAATCCACTTGCCTTTGAAGACGCTGTTGGAAAGCTTCTCTTTT 6581
Db 535 GGAAGCTTGATATCATCAATCCACTTGCCTTTGAAGACGCTGTTGGAAAGCTTCTCTTTT 476

Qy 6582 TCCACGATGTTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCATCT 6641
Db 475 TCCACGATGCTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGCAGAGGCATCT 416

Qy 6642 TGAACGATAGCCCTTCTTTATCGCAATGATGGCAATTTGTAGAAAGCCATCTTCTCTTTCT 6701
Db 415 TCAACGATGGCTTCTCTTTATCGCAATGATGGCAATTTGTAGAGCCACCTTCTCTTTCTC 356

Qy 6702 ACTGCTCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGAT 6761
Db 355 ACTATCTTTCACAAATAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGAT 296

Qy 6762 ATTACCCCTTTGTGAAAAGTCTCAATAGCCCTCTGCTCTCTGAGACTGTATCTTTTGATA 6821
Db 295 ATTACCCCTTTGTGAAAAGTCTCA----- 272

Qy 6822 TTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGATCTAGATATCACATCAA 6881
Db 271 -----CATCGGACCATCACATCAA 253

Qy 6882 TCCACTTGTGTAAGACGCTGTTGGAAGCTTCTTTTCCACGATGTTCTCGTGGGT 6941
Db 252 TCCACTTGTGTAAGACGCTGTTGGAAGCTTCTTTTCCACGATGTTCTCGTGGGT 193

Qy 6942 GGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAAACGATAGCCCTTCTCTTTA 7001
Db 192 GGGGGTCCATCTTTGGGACCACTGTCGGCAGAGGCATCTTCAACGATGGCTTCTCTTTA 133

Qy 7002 TCGCAATGATGGCAATTTGTAGAACCATCTTCTCTTTTCTACTGTCCTTTTCGATGAAGTGA 7061
Db 132 TCGCAATGATGGCAATTTGTAGAGCCACCTTCTCTTTTCCACTATCTTCACAATAAAGTGA 73

Qy 7062 CAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCTTTGTTGAAAGTCA 7121
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Qy 7122 TCA 7124
Db 12 TCA 10
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RESULT 13
US-09-737-698B-30/C
; Sequence 30, Application US/09737698B
; Patent No. 6462258
; GENERAL INFORMATION:
; APPLICANT: Finch, Karen
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6462258el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)C
; CURRENT APPLICATION NUMBER: US/09/737,698B
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/171,173
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 30
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1742)
; OTHER INFORMATION: chimeric promoter fusion CamV and Act2 polynucleotides + Act2 in
; OTHER INFORMATION: tro
US-09-737-698B-30

Query Match      5.0%; Score 379.2; DB 3; Length 1742;
Best Local Similarity 81.0%; Pred. No. 2.4e-64;
Matches 489; Conservative 0; Mismatches 38; Indels 77; Gaps 1;

Qy 6182 TCGGATCTAGATATCACATCAATCCACTTGCCTTTGAAGACGCTGTTGGAAAGCTTCTCTTTT 6241
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Qy 6242 TTCCACGATGTTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCATC 6301
Db 475 TTCCACGATGCTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGCAGAGGCATC 416

Qy 6302 TTGAACGATAGCCCTTCTCTTTATCGCAATGATGGCAATTTGTAGAAAGCCATCTTCTCTTTT 6361
Db 415 TTCAACGATGGCTTCTCTTTATCGCAATGATGGCAATTTGTAGAGCCACCTTCTCTTTTCT 356

Qy 6362 TACTGCTCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGA 6421
Db 355 CACTATCTTCAACAATAAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGA 296

Qy 6422 TATTACCCCTTTGTGAAAAGTCTCAATAGCCCTCTGCTCTCTGAGACTGTATCTTTTGAT 6481
Db 295 TATTACCCCTTTGTGAAAAGTCTCA----- 271

Qy 6482 ATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGATCTAGATATCACATCA 6541
Db 270 -----CATCGGACCATCACATCA 253

Qy 6542 ATCCACTTGTGTAAGACGCTGTTGGAAGCTTCTTTTCCACGATGTTCTCGTGGG 6601
Db 252 ATCCACTTGTGTAAGACGCTGTTGGAAGCTTCTTTTCCACGATGTTCTCGTGGG 193

Qy 6602 TGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCCTTCTCTTTT 6661
Db 192 TGGGGTCCATCTTTTGGGACCACTGTCGGCAGAGGCATCTTCAACGATGGCTTCTCTTTT 133

Qy 6662 ATCGCAATGATGGCAATTTGTAGAACCATCTTCTCTTTTCTACTGTCCTTTTCGATGAAGTG 6721
Db 132 ATCGCAATGATGGCAATTTGTAGAGCCACCTTCTCTTTTCCACTATCTTCACAATAAAGTG 73

Qy 6722 ACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCTTTGTTGAAAGT 6781
Db 72 ACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCTTTGTTGAAAGT 13

Qy 6782 CTCA 6785
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RESULT 14
US-09-737-626A-30/C
; Sequence 30, Application US/09737626A
; Patent No. 6660911
; GENERAL INFORMATION:
; APPLICANT: Finch, Karen
; APPLICANT: Flaszinski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6660911el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/09/737,626A
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
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; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 30
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1742)
; OTHER INFORMATION: chimeric promoter fusion CamV and Act2 in
; OTHER INFORMATION: tro
US-09-737-626A-30

Query Match 5.0%; Score 379.2; DB 3; Length 1742;
Best Local Similarity 81.0%; Pred. No. 2.4e-64;
Matches 489; Conservative 0; Mismatches 38; Indels 77; Gaps 1;
QY 6182 TCGGATCTAGATATCACATCAATCCACTTGGCTTTGAGACGTTGGAACTCTCTTT 6241
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QY 535 TTGAAGCTTGTATATCACATCAATCCACTTGGCTTTGAGACGTTGGAACTCTCTTT 476
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Db |||||
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Db |||||
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QY 6602 TGGGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCATCTTCAACGATGTTCTCTTT 6661
Db |||||
QY 192 TGGGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCATCTTCAACGATGTTCTCTTT 133
Db |||||
QY 6662 ATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCTACTGTCTTTTCGATGAAGTG 6721
Db |||||
QY 132 ATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCCACTATCTTCAATAAAGTG 73
Db |||||
QY 6722 ACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCGATATATACCTTTGTTGAAAAGT 6781
Db |||||
QY 72 ACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCGATATATACCTTTGTTGAAAAGT 13
Db |||||
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QY 12 CTCA 9

RESULT 15

US-10-427-169-30/C
; Sequence 30, Application US/10427169
; Patent No. 6919495
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flaszinski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6919495el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B

; CURRENT APPLICATION NUMBER: US/10/427,169
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/737,626A
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 30
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1742)
; OTHER INFORMATION: chimeric promoter fusion CamV and Act2 polynucleotides +
; OTHER INFORMATION: tro
US-10-427-169-30

Query Match 5.0%; Score 379.2; DB 3; Length 1742;
Best Local Similarity 81.0%; Pred. No. 2.4e-64;
Matches 489; Conservative 0; Mismatches 38; Indels 77; Gaps 1;
QY 6182 TCGGATCTAGATATCACATCAATCCACTTGGCTTTGAGACGTTGGAACTCTCTTT 6241
Db |||||
QY 535 TTGAAGCTTGTATATCACATCAATCCACTTGGCTTTGAGACGTTGGAACTCTCTTT 476
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QY 6362 TACTGTCTTTGCGAATGATGACATAGCTGGGCAATGGAAATCCGAGAGGTTTCCCGA 6421
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QY 6422 TATTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT 6481
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QY 270 -----CATCGGACCATCATCA 253
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QY 6542 ATCCACTTGTGTAAGACGTTGGTGAACGCTTCTTTTCCAGATGTTCTCGTGGG 6601
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QY 252 ATCCACTTGTGTAAGACGTTGGTGAACGCTTCTTTTCCAGATGTTCTCGTGGG 193
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QY 6602 TGGGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCATCTTGAACGATAGCTTTCTCTTT 6661
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QY 192 TGGGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCATCTTCAACGATGTTCTCTTT 133
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QY 6662 ATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCTACTGTCTTTTCGATGAAGTG 6721
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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	964.8	12.7	1320	4	CNS0A5O4
4	720.4	9.5	736	10	CW802337
5	711	9.4	720	10	CW797151
6	688.4	9.1	972	8	DR750042
7	672.2	8.9	868	8	DR749973
8	671.4	8.9	866	8	DR750041
9	570.2	7.5	733	8	CX308688
10	528	7.0	528	10	CNS00PNT
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12	461.2	6.1	486	9	B26529
13	442	5.8	452	9	AQ011657
14	431.4	5.7	433	9	B97814
15	424.8	5.6	468	10	CL517384
16	412.2	5.4	690	7	CF854584
17	381.2	5.0	655	7	CK437920
18	381.2	5.0	698	7	CK438348
19	381.2	5.0	698	7	CK438483
20	381.2	5.0	702	7	CO472768
21	381.2	5.0	713	7	CK437984
22	381.2	5.0	736	7	CK438485

C 23	381.2	5.0	741	7	CK438362
C 24	381.2	5.0	755	7	CK438332
C 25	381.2	5.0	803	7	CO472761
C 26	371	4.9	446	1	AA585745
C 27	350.2	4.6	492	9	AQ361936
C 28	336.2	4.4	839	9	AQ362115
C 29	324.6	4.3	441	7	CK437874
C 30	319.2	4.2	869	10	CW799882
C 31	315	4.1	610	7	CO481168
C 32	310	4.1	654	10	CG206846
C 33	305.4	4.0	557	8	CV961115
C 34	305.4	4.0	507	8	CV965337
C 35	305.4	4.0	609	8	CV965230
C 36	305.4	4.0	692	8	CV964956
C 37	304.6	4.0	490	9	BZ586494
C 38	304.6	4.0	534	9	BZ586497
C 39	304.6	4.0	570	9	BZ586953
C 40	304.6	4.0	741	10	CZ908574
C 41	304.4	4.0	643	10	CG805032
C 42	303.8	4.0	431	9	BH753412
C 43	303.6	4.0	385	9	BH212594
C 44	303.6	4.0	435	9	BH171104
C 45	303.6	4.0	438	9	BH619277

ALIGNMENTS

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LOCUS
DEFINITION
CNS0A60U 1466 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTFB52B04 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

2 (bases 1 to 1466)
Unpublished
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Matches 1274; Conservative 0; Mismatches 11; Indels 1; Gaps 1;									
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QY	4165	CTTACGGCAGCTCTCATCACCACCGACTTCTCAGGTTGCAGGTTCCGAGTCAAGCTAGAGT	4224						
DB	233	CTTACGGCAGCTCTCATCACCACCGACTTCTCAGGTTGCAGGTTCCGAGTCAAGCTAGAGT	292						
QY	4225	GAATTCATGTGGAAACGTGCTCGGATCGCAAAAGTCCCATTTGCCCTGAAGCAGCTCTAAA	4284						
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DB	353	TTGCCCTAGATGTGACTCAACCAATCTAAAGTTCTGTACTTCAATAATATAGCTTAC	412						
QY	4345	TCAACTCGCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTCGGCGTTCTCTTGAG	4404						
DB	413	TCAACTCGCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTCGGCGTTCTCTTGAG	472						
QY	4405	GAATGTTCTGTGTGAGGAGGCTTTAGGAGGAACAAGAGACCAATCCAGATCGAAATC	4464						
DB	473	GAATGTTCTGTGTGAGGAGGCTTTAGGAGGAACAAGATAAGCAATCCAGATCGAAATC	532						
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QY	4525	TTACTCAAAACCCCTAGCAAGTTTTCATAGCTACGGTCAAAATCCCGGAGTTTAATTCCAACTT	4584						
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QY	4585	GCCCATCTTGCTCTCTCCAAAGCCTTGGAGATTACAAATCAAGCAACACTGGATTAGA	4644						
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QY	4825	TAATCAAGTGATTTCTCAACAGAGTAGTGTATTTCCATCAGCTAAATGTTTAAGCC	4884						
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QY	5005	TTTGGGTAATATCAACATAAACTCAGGCAGGAACGAGGAATACATCATCGGGAGGTAA	5064						
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DB	1432	ATATTGGCTATATATAGAGGTGTGGG	1457						
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone									
GSLTFB532B03 of Flowers and buds of strain col-0 of Arabidopsis									
thaliana (thale cress).									
ACCESSION BX822618									
VERSION 1 GI:42463912									
KEYWORDS HTC; GSLT cDNA									
SOURCE Arabidopsis thaliana (thale cress)									
ORGANISM Arabidopsis thaliana									
REFERENCE 1 (bases 1 to 1371)									
AUTHORS Castellani,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,									
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,									
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.									
TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:									
A Combined Approach to Evaluate and Improve Arabidopsis Genome									
JOURNAL Annotation									
REFERENCE 2 (bases 1 to 1371)									
AUTHORS Genoscope.									
JOURNAL Direct Submission									
COMMENT Submitted (18-NOV-2003) Genoscope - Centre National de Sequenage :									
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr									
- Web : www.genoscope.cns.fr)									
The sequences are based on single pass reads.									
Life Technologies (a division of Invitrogen)									
full-length libraries construction : Temple G.									
Genoscope members carried out sequencing and annotation : Castelli									
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,									
Schachter V., Weissenbach J., Salanoubat M.									
URV INRA : Clepet C., Caboche M.									
Annotation is based on the June 2003 version of the Arabidopsis									
genome released by MIPS (Munich Information center for Protein									
Sequences). 5 prime and 3 prime are assembled with Phrap.									
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Best Local Similarity 92.9%; Pred. No. 1.5e-188;
Matches 1221; Conservative 0; Mismatches 0; Indels 93; Gaps 1;

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QY 4825 TAATCAAGTGTATCTCAACAGAGTAGTGTATTATTCCAATCAGCTAAATGTTTAAGCC 4884
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DEFINITION
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  79-1021445-065-006-G10-SeqB MP12-ADIS-065d Arabidopsis thaliana
  cDNA clone 006-G10, mRNA sequence.
ACCESSION
  DR750042
VERSION
  DR750042.1 GI:71035382
KEYWORDS
  Arabidopsis thaliana (thale cress)
ORGANISM
  Arabidopsis thaliana

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B.,
Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R.,
Engstroem, D., Martin, C., Angenot, G.C., Baeumlein, H., Mock, H.P.,
Carbenero, P., Colombo, L., Tonelli, C., Engstroem, P.,
Droge-Laser, W., Gatz, C., Kavanagh, T., Kuhnir, S., Zabeau, M.,
Lau, T., Hordsworth, M., Ruberti, I., Ratcliff, P., Smeekens, S.,
Somssich, I., Weishaar, B. and Traas, J.
REGIA, an EU project on functional genomics of transcription
factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002)
Contact:
Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski,
Engstroem, Droge-Laser, Gatz, Kavanagh, Kuhnir, Zabeau, Lau, Hordsworth,
Ruberti, Smeekens, Somssich, Weishaar, Traas
Bielefeld University, Institute for Genome Research
Universitaetstrasse 25, D-33594 Bielefeld, Germany
Email: bernd.weishaar@uni-bielefeld.de
AGI: AT3G5370; SeqAnalysis: truncated in 5' at pos 179;
Translation: no full cds detected

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Data analysis performed in the frame of REGULATORS (Exploiting
inter-species conservation in promoter sequences to identify
regulators of reproductive development and physiological
performance), a Trilateral Co-Operation in Plant Genomics between
Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by
G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent
Thareau (TBP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and
Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE,
lecharny-ad-ibp.u-psud.fr).

```

```

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TIGRVS annotation, and the resulting AGI code is presented if more
than 90 percent identity was found. The sequences were also blasted
against all TIGRVS introns, and matches longer than 50 bp with 95
percent identity are reported as 'intron found'. The remaining
terms for SeqAnalysis describe the outcome of the evaluation of the
CDS detected after pairwise alignment with CDS plus pseudogenes
from the TIGRVS annotation file. The sequences or contigs for which
a full CDS with or without STOP codon was detected, a BLASTp
against all TIGRVS protein sequences was performed. Full perfect:
100 percent identity; full good: better than 95 percent identity
over more than 95 percent of the sequence; partial good: better
than 95 percent identity over less than 95 percent of the sequence;
weak similarity: less than 95 percent identity over less than 95

```

```

percent of the sequence; no similarity: no hit from BLASTp. Note
that the collection contains a few clones for which sequencing was
not successful, which could have simple technical reasons.
Obviously, information about these clones is missing in the
submitted data.

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Seq primer: SeqB GTAACATCAGAGATTTTGAGACAC.
Insert length: 972 Std Error: 0.00

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FEATURES

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  /note="Vector: pDONR201; In the context of the EU-funded
  project REGIA (QLG-CT11999-00876, coordinator Javier
  Paz-Ares), a set of transcription factor ORFs was
  generated. The ORFs were produced in a decentralized way
  in the labs of the participants. Most of the ORFs were
  generated by RT-PCR using cDNA from various A. thaliana
  tissues as a template. Initially, it was planned to use
  yeast recombination to move the ORFs from the cloning
  vectors into target constructs. For this reason, a number
  of the clones contain 'REGIA tags' (RG_tag1:
  5pr-AATTCAGCTCACCACG-3pr; RG_tag2:
  5pr-CATGGCAATTCGGGATC-3pr). During the lifetime of the
  project, the GATEWAY system became available and finally
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  of the REGIA project, the clones were collected as plasmid
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  MPI of Plant Breeding Research (ADIS; head: Bernd
  Weishaar), the plasmids were re-transformed into
  DH5alpha, arrayed into 96-well plates and new plasmid DNA
  was prepared. Re-transformation proved to be difficult
  because a number of clones displayed poor growth. Data
  submission has been handled by GABIpD
  (http://gabi.rzpd.de)."

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ORIGIN

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Query Match          9.1%; Score 688.4; DB 8; Length 972;
Best Local Similarity 89.4%; Pred. No. 4.5e-112;
Matches 792; Conservative 0; Mismatches 1; Indels 93; Gaps 1;

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QY 4293 GATGTGACTCAACCAATTAAGTTCCTGTTACTTCAATACTATAGCCTTACTCAACCTC 4352
DB 828 GATGTGACTCAACCAATTAAGTTCCTGTTACTTCAATACTATAGCCTTACTCAACCTC 769
QY 4353 GCCATTTCTGCAAAACATGTCGTCTATTGGACACGCTGGCGGTTCTTTGAGGAATGTTTC 4412
DB 768 GCCATTTCTGCAAAACATGTCGTCTATTGGACACGCTGGCGGTTCTTTGAGGAATGTTTC 709
QY 4413 CTGTGGAGGAGGCTTTAGGAGGAACAAGAGAGCAATTCAGATCGAAATCTAGCGTCG 4472
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DB 588 ACCCTAGCAAGTTCATAGTACGCTCAAAATCCCGGAGTTTAAATCCCACTTGCCCATCT 529
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DB 528 TGCCTCTCTCCAAAGCCTTGGAGATTACAATTAAGCAACACTGGATTAGATTTGGTG 469

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DEFINITION cDNA clone 006-G10, mRNA sequence.
ACCESSION DR749973
VERSION DR749973.1 GI:71035313
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
```

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REFERENCE
AUTHORS Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B.,
Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R.,
Coupland, G., Martin, C., Angenent, G.C., Baumeister, H., Mock, H.P.,
Carbonero, P., Colombo, L., Tonelli, C., Engstrom, P.,
Droge-Laser, W., Gatz, C., Kavanagh, T., Kuschir, S., Zabeau, M.,
Lau, T., Hordsworth, M., Ruberti, I., Ratcliff, F., Smeekens, S.,
Somsich, I., Weisshaar, B. and Traas, J.
TITLE REGIA, an EU project on functional genomics of transcription
factors from Arabidopsis thaliana
JOURNAL Comp. Funct. Genomics 3 (2), 102-108 (2002)
COMMENT Contact:
Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski,
Engstrom, Droge-Laser, Gatz, Kavanagh, Kuschir, Zabeau, Lau, Hordsworth,
Ruberti, Smeekens, Somsich, Weisshaar, Traas
Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Email: bernd.weisshaar@uni-bielefeld.de
AGI: AT3G5370; SeqAnalysis: truncated in 5' at pos 179;
Translation: no full cds detected
```

```
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inter-species conservation in promoter sequences to identify
regulators of reproductive development and physiological
performance), a Trilateral Co-Operation in Plant Genomics between
Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by
```

G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE, lecharny-ad-ibp.u-psud.fr).

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Insert Length: 868 Std Error: 0.00
Seq primer: SELTA TCGCGTTAACGTCAGTCATGATCTC.

FEATURES

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/lab_host="E. coli DH5alpha"
/clone_lib="MP1Z-ADIS-065d"
/note="Vector: pDONR201; In the context of the EU-funded project REGIA (OLG-CTL1999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag1: 5pr-AATTCAGCTCACACC-3pr; RG_tag2: 5pr-CATGGCAATCCCGGATC-3pr). During the lifetime of the project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS; head: Bernd Weisshaar), the plasmids were re-transformed into DH5alpha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GABI (http://gabi.rzpd.de)."

ORIGIN

Query Match 8.9%; Score 672.2; DB 8; Length 868;
Best Local Similarity 88.8%; Fred. No. 3.5e-103;
Matches 788; Conservative 0; Mismatches 5; Indels 94; Gaps 2;
QY 4233 TGGTGAACGCTCGGATCGCAAAAGTCCCATTCCTTGAAGCAGCTCTAAATGCCCTA 4292
|||||
Db 73 TGGTGAACGCTCGGATCGCAAAAGTCCCATTCCTTGAAGCAGCTCTAAATGCCCTA 132
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Db 133 |GATGTGACTCAACCAATACTAAGTCTCTGTTACTTCAATAAATATATAGCCTTACTCAACCTC 192
QY 4353 |GCCATTTCTGCAAAACATGTCGCTATTGGACACGTTGGGGTTCCTTGGAGGAATGTC 4412
Db 193 |GCCATTTCTGCAAAACATGTCGCTATTGGACACGTTGGGGTTCCTTGGAGGAATGTC 252
QY 4413 |CTGTTGGAGGAGGCTTTAGGAGGAACAGAGAAAGCAAAATCCAGATCGAAATCTACGGTCG 4472
Db 253 |CTGTTGGAGGAGGCTTTAGGAGGAACAGAGAAAGCAAAATCCAGATCGAAATCTACGGTCG 312
QY 4473 |TGGTCTCGACTGATAATACTACTAGTACTTATCATCTTACTTCTGCGCCCAAGTTACTCAA 4532
Db 313 |TGGTCTCGACTGATAATACTACTAGTACTTATCATCTTACTTCTGCGCCCAAGTTACTCAA 372
QY 4533 |ACCTAGCAAGTTTTCATAGCTACGCTCAATCCCGGAGTTTAATTCACACTTGCCCATCT 4592
Db 373 |ACCTAGCAAGTTTTCATAGCTACGCTCAATCCCGGAGTTTAATTCACACTTGCCCATCT 432
QY 4593 |TGCTCTCTCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGATTGTTGGTG 4652
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VERSION
  DR750041.1
KEYWORDS
  GI:71035381
SOURCE
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  Arabidopsis thaliana
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  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  1 (bases 1 to 866)
REFERENCE
  Paz-Ares,J., Valencia,A., Costantino,P., Vittorioso,P., Davies,B.,
  Gilmartin,P., Giraudat,J., Parcy,F., Reindl,A., Sablowski,R.,
  Coupland,G., Martin,C., Angenent,G.C., Baeumlein,H., Mock,H.P.,
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Carbonero,P., Colombo,L., Tonelli,C., Engstrom,P.,
Droegge-Laser,W., Gatz,C., Kavanagh,T., Kushmir,S., Zabeau,M.,
Lau,T., Holdsworth,M., Ruberti,I., Ratcliff,F., Smeekens,S.,
Somssich,I., Weisshaar,B. and Traas,J.
REGIA, an EU project on functional genomics of transcription
Comp. Funct. Genomics 3 (2), 102-108 (2002)

Contact:
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Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Email: bernd.weisshaar@uni-bielefeld.de

AGI: AT3055370; SeqAnalysis: truncated in 5' at pos 179;
Translation: no full cds detected
Data analysis performed in the frame of REGULATORS (Exploiting inter-species conservation in promoter sequences to identify regulators of reproductive development and physiological performance), a Trilateral Co-Operation in Plant Genomics between Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE, lecharny-ad-ibp.u-psud.fr).

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Insert Length: 866 Std Error: 0.00
Seq primer: Sela TCGCGTTAAGCTAGCATGATCTC.

Location/Qualifiers
1..866
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="GABI:1452132"
/db_xref="taxon:3702"
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/lab_host="E. coli DH5alpha"
/clone_lib="MP1Z-ADIS-065d"
/note="Vector: pDONR201; In the context of the EU-funded project REGIA (QLG-CT11999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag1: Spr-AATTCCAGCTCACACC-3pr; RG_tag2: 5pr-CATGGCAATTCCCGGATC-3pr). During the lifetime of the

project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS; head: Bernd Weishaar), the plasmids were re-transformed into DH5alpha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GabiPD (<http://gabi.rzpd.de>)."

ORIGIN

Query Match 8.9%; Score 671.4; DB 8; Length 866;
Best Local Similarity 88.1%; Pred. No. 4.8e-109;
Matches 781; Conservative 0; Mismatches 12; Indels 93; Gaps 1;

QY 4233 TGGTGGAGGCTCGGATCGCAAAAGTCCCAAGTCCCTGGAAGCAGCTCTAAATGCCCTA 4292
DB 18 TGGNGGACCTTGAAGAAGTCGCAAAAGTCCCAAGTCCCTGGAAGCAGCTCTAAATGCCCTA 77

QY 4293 GATGTGACTCAACCAATCTAGTCTCTGTTACTTCAATAACTATAGCCTTACTCAACCTC 4352
DB 78 GATGTGACTCAACCAATCTAGTCTCTGTTACTTCAATAACTATAGCCTTACTCAACCTC 137

QY 4353 GCCATTTCTGAAAAATGCTGCTGCTATTTGACACGTCGGCGGTTCTTTGAGGAATGTTT 4412
DB 138 GCCATTTCTGAAAAATGCTGCTGCTATTTGACACGTCGGCGGTTCTTTGAGGAATGTTT 197

QY 4413 CTGTTGGAGGAGCTTTAGGAGACAGAGAGCAAAATCCAGATCGAAATCTACGTCG 4472
DB 198 CTGTTGGAGGAGCTTTAGGAGACAGAGAGCAAAATCCAGATCGAAATCTACGTCG 257

QY 4473 TGGTCTCGACTGATAATCTAGTACTTCTATCTACTTCTCGCCCAAGTTACTCAA 4532
DB 258 TGGTCTCGACTGATAATCTAGTACTTCTATCTACTTCTCGCCCAAGTTACTCAA 317

QY 4533 ACCCTAGCAAGTTTCATAGCTACGTCAAATCCCGAGTTTAATTCACATTTGCCATCT 4592
DB 318 ATTTTGTAGCAAGTTTCATAGCTACGTCAAATCCCGAGTTTAATTCACATTTGCCATCT 377

QY 4593 TGCCTCTCTCAAAAGCTTGGAGATACAAATTCAGCAACACTGGATAGATTTTGGTG 4652
DB 378 TGCCTCTCTCAAAAGCTTGGAGATACAAATTCAGCAACACTGGATAGATTTTGGTG 437

QY 4653 GAATCAAAATAGCAACATGATAAGTGGTATGATCTTCTAGTCTGGATCTTGGATGAT 4712
DB 438 GAATCAAAATAGCAACATGATAAGTGGTATGATCTTCTAGTCTGGATCTTGGATGAT 497

QY 4713 GGAGAATACCTCCATCACAACAGCTCAGCAATTCCTTTCTTTGATCAACACTACCGAT 4772
DB 498 GGAGAATACCTCCATCACAACAGCTCAGCAATTCCTTTCTTTGATCAACACTACCGAT 557

QY 4773 TGGTGCATCTTCAACCGGTTATATCAATTTACTAGAGGTGAAGGAGTGTATATCAAG 4832
DB 558 TGGTGCATCTTCAACCGGTTATATCAATTTACTAGAGGTGAAGGAGTGTATATCAAG 594

QY 4833 GTGATTTCTCAACAGAGAGTAGTATTTATTCATCAGCTAATGTTTAAGCCCTTGATGG 4892
DB 595 GTGATTTCTCAACAGAGAGTAGTATTTATTCATCAGCTAATGTTTAAGCCCTTGATGG 594

QY 4893 ATTTTCTTTTTCAGCGGGGTTAGCGCCAGCAAAAGAAATGTGAAGCGGGAAGAAATG 4952
DB 595 ATTTTCTTTTTCAGCGGGGTTAGCGCCAGCAAAAGAAATGTGAAGCGGGAAGAAATG 644

QY 4953 ATCAGATCGGGGTAGGATAGGGATGAGATGAATTAATTAATCAAGAAATCTTTTGGGTA 5012
DB 645 ATCAGATCGGGGTAGGATAGGGATGAGATGAATTAATTAATCAAGAAATCTTTTGGGTA 704

QY 5013 ATATCAACATAACTCAGGAGGAGGAGGATACATCATCTGCGGAGGTAACTTCTT 5072
DB 705 ATATCAACATAACTCAGGAGGAGGAGGATACATCATCTGCGGAGGTAACTTCTT 764

QY 5073 GGACGGTTTTCACCTCCCAACCACTCAACAGGCCATCTCTCATTTCTA 5118
DB 765 GGACGGTTTTCACCTCCCAACCACTCAACAGGCCATCTCTCATTTCTA 810

RESULT 9
LOCUS CX308688/c 733 bp mRNA linear EST 06-MAY-2005
DEFINITION C21002G02Rv AbsLeaSub1 Citrus clementina cDNA clone C21002G02, mRNA sequence.
ACCESSION CX308688
VERSION CX308688
KEYWORDS CX308688.1 GI:63077542
SOURCE EST.
ORGANISM Citrus clementina
Clementina
REFERENCE 1 (bases 1 to 733)
AUTHORS Forment, J., Gadea, J., Huerta, L., Abizanda, L., Agusti, J., Alamar, S., Alos, E., Andres, F., Arribas, R., Beltran, J. P., Berbel, A., Blazquez, M. A., Brumos, J., Canas, L. A., Cercos, M., Colmenero-Flores, J. M., Conesa, A., Establies, B., Gandia, M., Garcia-Martinez, J. L., Gimeno, J., Gisbert, A., Gomez, G., Gonzalez-Candelas, L., Granel, A., Guerri, J., Lafuente, M. T., Madueno, F., Marcos, J. F., Marques, M. C., Martinez, F., Martinez-Godoy, M. A., Miralles, S., Moreno, P., Navarro, L., Pallas, V., Perez-Amador, M. A., Perez-Vall, J., Pons, C., Rodrigo, I., Rodriguez, P. L., Royo, C., Serrano, R., Soler, G., Tadeo, F., Talon, M., Terol, J., Trenor, M., Vaello, L., Vicente, O., Vidal, Ch., Zacarias, L. and Conejero, V.

TITLE Development of a citrus genome-wide EST collection and cDNA microarray as resources for genomic studies
JOURNAL Plant Mol. Biol. 57 (3), 375-391 (2005)
PUBMED 15830128
COMMENT Contact: Forment J
Genomics Laboratory
Instituto de Biologia Molecular y Celular de Plantas (Universidad Politecnica de Valencia - Consejo Superior de Investigaciones Cientificas)
Avenida de los Naranjos s/n, 46022 Valencia, Spain
Email: jforment@ibmcp.upv.es.
Location/Qualifiers
1. 733
/organism="Citrus clementina"
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/db_xref="taxon:95681"
/clones="C21002G02"
/sex="hermaphrodite"
/dev_stage="adult trees"
/lab_host="Escherichia coli"
/clone_lib="AbsLeaSub1"
/note="Organ: leaves; Vector: pCR2.1; Subtracted cDNA library made from laminar abscission zone of leaves"

FEATURES
source
1. 733

ORIGIN
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Best Local Similarity 92.5%; Pred. No. 5e-91;
Matches 615; Conservative 0; Mismatches 38; Indels 12; Gaps 1;

QY 6190 AGATATCATCATCAATCCACTTGTGTTGAAGACGTGGTTGGAAACGTCTTTTTCACGA 6249
DB 679 AGATATCATCATCAATCCACTTGTGTTGAAGACGTGGTTGGAAACGTCTTTTTCACGA 620

QY 6250 TGTTCCTCGTGGTGGGGTCCATCTTTGGACCACTGTGGTAGAGGATCTTGAACGA 6309
DB 619 TGTTCCTCGTGGTGGGGTCCATCTTTGGACCACTGTGGTAGAGGATCTTGAACGA 560

QY 6310 TAGCCTTCTCTTTATCGCAATGATGGCATTTGTAGAAGCATCTTCTTTTCTACTGTCC 6369
DB 559 TGGCCTTCTCTTTATCGCAATGATGGCATTTGTAGAAGCATCTTCTTTTCTACTGTCT 500

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QY 6370 TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 6429
Db 499 TCACAAATAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCGATATTACCC 440
QY 6430 TTTGTTGAAAAGTCTCAATAGACCCCTCGGTCTTCTGAGACTGTATCTTTTGATATCTTTGG 6489
Db 439 TTTGTTGAAAAGTCTCAATAGACCCCTCGGTCTTCTGAGACTGTATCTTTTGATATTTTGG 380
QY 6490 AGTAGACAGAGTGTGCTGCTCCACCATGTTGGGGATCTAGATATCATCAATCCACTT 6549
Db 379 AGTAGACAAGTGTGCTGCTCCACCATGT-----TATCACATCAATCCACTT 332
QY 6550 GCTTTGAAAGACTGTGCGAAGCTCTCTTTTCCACGATGTCTCGTGGGTGGGGGTC 6609
Db 331 GCTTTGAAAGACTGTGCGAAGCTCTCTTTTCCACGATGTCTCGTGGGTGGGGGTC 272
QY 6610 CATCTTTGGGACCACCTGTCGCTGAGGAGCATCTTGAACGATAGCCCTTCTTTATGCGCAAT 6669
Db 271 CATCTTTGGGACCACCTGTCGCGAGAGGCATCTTCAACGATGGCCCTTCTTTATGCGCAAT 212
QY 6670 GATGCAATTTGAGAAGCATCTTCTTTCTACTGTCTCTTCGATGAAGTGACAGATAG 6729
Db 211 GATGCAATTTGAGAAGCATCTTCTTTCTCACTATCTTCAATATAAAGTGACAGATAG 152
QY 6730 CTGGGCAATGGAATCCGAGGAGGTTTCCGATATTACCTTTGTTGAAAAGTCTCAATAG 6789
Db 151 CTGGGCAATGGAATCCGAGGAGGTTTCCGATATTACCTTTGTTGAAAAGTCTCAATAG 92
QY 6790 CCTCTGCTCTTCTGAGACTGTATCTTTGATATTTCTGGAGTGAAGAGTGTCGTCT 6849
Db 91 CCTCTGCTCTTCTGAGACTGTATCTTTGATATTTCTGGAGTGAAGAGTGTCGTCT 32
QY 6850 CCACC 6854
Db 31 CCACC 27
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RESULT 10
CNS00PNT 528 bp DNA linear GSS 28-JUN-1999
LOCUS Arabidopsis thaliana genome survey sequence T7 end of BAC F9G12 of
DEFINITION IGF library from strain Columbia of Arabidopsis thaliana, genomic
survey sequence.
ACCESSION AL084743
VERSION AL084743.1 GI:5285883
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 528)
AUTHORS Salanoubat,M., Choisme,N., Artiguenave,F., Brottier,P., Wincker,P.,
Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 528)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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1..528
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/db_xref="taxon:3702"
/clone="F9G12"
/clone_lib="IGF"
/ecotype="Columbia"
/note="end : T7"
ORIGIN
Query Match 7.0%; Score 528; DB 10; Length 528;
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Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2007 TTTATTTTGTAAAGGCATTTTCTTAAACAGAGGAATTTTACATCATCTTTAGACTGA 2066
Db 1 TTTATTTTGTAAAGGCATTTTCTTAAACAGAGGAATTTTACATCATCTTTAGACTGA 60
QY 2067 ACTTTCCGGATAAAAAATCTGCCATGCAAAAGGTAATTTATTTTTCATGACAAAAAGCCA 2126
Db 61 ACTTTCCGGATAAAAAATCTGCCATGCAAAAGGTAATTTATTTTTCATGACAAAAAGCCA 120
QY 2127 CAATGGCGATAAATTAATACTATAATACTATGCAAAAAAGAACTTTTACCTTGGGTCAATCCG 2186
Db 121 CAATGGCGATAAATTAATACTATAATACTATGCAAAAAAGAACTTTTACCTTGGGTCAATCCG 180
QY 2187 AGGAAAAAAGGTACACTCGATTGTGCAACTCCCAAGAGACACCCCACTACCAATT 2246
Db 181 AGGAAAAAAGGTACACTCGATTGTGCAACTCCCAAGAGACACCCCACTACCAATT 240
QY 2247 CACCTTTATTTGTTTCTTTTATTTCACTCAAAATCTTTTAAATTTTAAATTAATTTCAATT 2306
Db 241 CACCTTTATTTGTTTCTTTTATTTCACTCAAAATCTTTTAAATTTTAAATTAATTTCAATT 300
QY 2307 ATTGCTTCTCTCGTTGTTTAAACCTTTTAAATTAATAAATGAAAGAGGTGCTAGGG 2366
Db 301 ATTGCTTCTCTCGTTGTTTAAACCTTTTAAATTAATAAATGAAAGAGGTGCTAGGG 360
QY 2367 TTTCTCTCTGCAATGCGCACTCTCGCTCTTCACATCTTTTGGGACCATTTGTTAAC 2426
Db 361 TTTCTCTCTGCAATGCGCACTCTCGCTCTTCACATCTTTTGGGACCATTTGTTAAC 420
QY 2427 GTATGCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 2486
Db 421 GTATGCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 480
QY 2487 TGTCGTTTCTCTCATAAAGAAATTTATTTAAACTTATTTTAGTCCAA 2534
Db 481 TGTCGTTTCTCTCATAAAGAAATTTATTTAAACTTATTTTAGTCCAA 528
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RESULT 11
CG729372/c 597 bp DNA linear GSS 20-OCT-2003
LOCUS 111911D07.Y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
DEFINITION CG729372 survey sequence.
ACCESSION CG729372
VERSION CG729372.1 GI:37771010
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 597)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 111911 row: 2
Class: transposon-tagged.
FEATURES
Location/Qualifiers
source
1..597
/organism="Zea mays"
/mol_type="genomic DNA"
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/db_xref="taxon:4577"
/tissue_type="leaf"
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/dev_stage="adult"
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/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmndb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
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ORIGIN

```
Query Match 6.3%; Score 477.4; DB 10; Length 597;
Best Local Similarity 90.8%; Pred. No. 1.6e-74;
Matches 524; Conservative 0; Mismatches 41; Indels 12; Gaps 1;

QY 6284 ACTGTCGGTAGGCGATCTTGAACGATAGCCCTTCTTATCGCAATGATGGCATTTGTA 6343
DB ACTGTCGGTAGGCGATCTGCAACGATGSCCTTCTTATCGCAATGATGGCATTTGTA 538
QY 6344 GAAGCCATCTTCTTTTACTGTCCTTTCGATGAGTGACAGATAGCTGGGCAATGGAA 6403
DB GGAGGCTCTGCTTTTCCACTATCTTCCAAATAAAGTGACAGATAGCTGGGCAATGGAA 478
QY 6404 TCCGAGGAGGTTTCCCGATATTACCTTTGTTGAAAGTCTCAATAGCCCTCTGCTCTC 6463
DB TCCGAGGAGGTTTCCCGATATTACCTTTGTTGAAAGTCTCAATAGCCCTTTGCTCTC 418
QY 6464 TGAGACTGTATCTTTGATATCTTGGAGTAGAGAGTGCTGCTCCACCATGTTGGG 6523
DB TGAGACTGTATCTTTGATATCTTGGAGTAGAGAGTGCTGCTCCACCATGCT --- 362
QY 6524 GATCTAGATATCATATCAATCCATTGCTTTGAAGACGTTGGTGAAGCGTCTTTTTC 6583
DB -----TATCATCATCAATCCATTGCTTTGAAGACGTTGGTGAAGCGTCTTTTTC 310
QY 6584 CACGATGTTCTCGTGGGGTCCATCTTTTGGGACCACTGCTCGTAGAGGCATCTTG 6643
DB CACGATGTTCTCGTGGGGTCCATCTTTTGGGACCACTGCTCGTAGAGGCATCTTG 250
QY 6644 AACGATAGCTTTCTCTTATCGCAATGATGGCAATTTGTAGAGCCATCTTCTTTTCTAC 6703
DB AACGATAGCTTTCTCTTATCGCAATGATGGCAATTTGTAGAGCCATCTTCTTTTCCAC 190
QY 6704 TGTCCTTTTCGATGGAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCGATAT 6763
DB TATCTTTCACATATAAGTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCGATAT 130
QY 6764 TACCTTTTGGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATT 6823
DB TACCTTTTGGAAAGTCTCAATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATT 70
QY 6824 CTTGAGTAGAGGAGTGCTGCTGCTCCACCATGTTG 6860
DB TTTGAGTAGAGGAGTGCTGCTGCTCCACCATGTTG 33
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RESULT 12

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B26529
LOCUS B26529 486 bp DNA linear GSS 13-OCT-1997
DEFINITION F9G12TF IGF Arabidopsis thaliana genomic clone F9G12, genomic
survey sequence.
ACCESSION B26529
VERSION B26529.1 GI:2512495
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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RESULT 13

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REFERENCE
AUTHORS Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D. and
Venter,J.C.
TITLE Use of a BAC End Sequence Database To Identify Minimal Overlaps for
Arabidopsis Genomic Sequencing
JOURNAL Unpublished (1997)
COMMENT Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Class: BAC ends
Seq primer: M13-21
High quality sequence stop: 486.
FEATURES
source
location/Qualifiers
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Produced by Thomas Altman"
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Query Match 6.1%; Score 461.2; DB 9; Length 486;
Best Local Similarity 98.1%; Pred. No. 1.3e-71;
Matches 477; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2024 ATTTTCTTAAACAGAGGAATTTTACATCATCTTTAGACTGAACCTTTCGGGATAAAAA 2083
DB 1 ATTTTGGTCTTAAACAGAGGAATTTTACATCATCTTTAGACTGAACCTTTCGGGATAAAAA 60
QY 2084 TCTGCCATGCAAAAGGTAATTTATTTTTCATGACAAAAGCCACAAATGGCGATAATATA 2143
DB 61 TCTGCCATGCAAAAGGTAATTTATTTTTCATGACAAAAGCCACAAATGGCGATAATATA 120
QY 2144 ACTATAATATATGCAAAACGAAACTTTTACCTTGGGTCTATACCGAGGAAAAACAAAGGTACA 2203
DB 121 ACTATAATATATGCAAAACGAAACTTTTACCTTGGGTCTATACCGAGGAAAAACAAAGGTACA 180
QY 2204 CTCGATTGTGACAACTCCACCAAGACCCACCTACCAATTCACCTTTATTTCTTCT 2263
DB 181 CTCGATTGTGACAACTCCACCAAGACCCACCTACCAATTCACCTTTATTTCTTCT 240
QY 2264 TTATTTCACTCAAAATCTTTTAAATTTTAAATTAATTAATTAATTCCTCTCTGTTG 2323
DB 241 TTATTTCACTCAAAATCTTTTAAATTTTAAATTAATTAATTAATTCCTCTCTGTTG 300
QY 2324 TTTTAAACCTTTTAAATTAATAAATGAAAGAGGTGCTAGGGTTTCTCTCTGATGG 2383
DB 301 TTTTAAACCTTTTAAATTAATAAATGAAAGAGGTGCTAGGGTTTCTCTCTGATGG 360
QY 2384 CCACCTCTGCTCTTACATCTTTTGGGACCACTTTTAAACGATATGCAAAAAA 2443
DB 361 CCACCTCTGCTCTTACATCTTTTGGGACCACTTTTAAACGATATGCAAAAAA 420
QY 2444 AAAAAAATAAAACCTT-ACATGCTAAGAAAACTCTCTTCTTCTTGTGTTCTCTCATATA 2502
DB 421 GTAATAAAGTAAACCTTAACTAATGCTAAGAAAACTCTCTTCTTGTGTTCTCTCATATA 480
QY 2503 AAAGAA 2508
DB 481 AAAGAA 486
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AQ011657 452 bp DNA linear GSS 29-MAY-1998
LOCUS F24E16TFB IGF Arabidopsis thaliana genomic clone F24E16, genomic
DEFINITION survey sequence.
ACCESSION AQ011657
VERSION AQ011657.1 GI:3166407
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 452)
AUTHORS Rounsley, S.D., Suh, E.J., Wible, C., Golden, K., Shatsman, S., Choi, P.,
Yu, K., Akinretaye, B., Shen, K., Goonasekaram, S., Militscher, J.,
Adams, M.D. and Venter, J.C.
TITLE A BAC End Sequence Database for Identifying Minimal Overlaps in
Arabidopsis Genomic Sequencing. Update 4
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: F24E16TR
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
High quality sequence stop: 452.
Location/Qualifiers
1..452
/organism="Arabidopsis thaliana"
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/sex="hermaphrodite"
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Produced by Thomas Altmann"
ORIGIN
Query Match 5.8%; Score 442; DB 9; Length 452;
Best Local Similarity 98.9%; Pred. No. 3.3e-68;
Matches 445; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4231 AATGGTGAACGTGCTCGGATCGCAAAAGTCCCATTTGCTGAAGCAGCTCTAAATTTGCC 4290
DB 3 AATGGTGGCAGCTGCTCGGATCGCAAAAGTCCCATTTGCTGAAGCAGCTCTAAATTTGCC 62
QY 4291 TAGATGTGACTCAACCACTAAGTCTGTGTACTTCAATACTATAGCCTTACTCAACC 4350
DB 63 TAGATGTGACTCAACCACTAAGTCTGTGTACTTCAATACTATAGCCTTACTCAACC 122
QY 4351 TCGCCATTTCTGCAAAAANGTCGTGCTATTGGACACGTGCGGTTCTTCGAGAAATGT 4410
DB 123 TCGCCATTTCTGCAAAAANGTCGTGCTATTGGACACGTGCGGTTCTTCGAGAAATGT 182
QY 4411 TCCTGTTGGAGGAGCTTTAGGAGGAACAAGAGAGCAATCCAGATCGAAATCTACGGT 4470
DB 183 TCCTGTTGGAGGAGCTTTAGGAGGAACAAGAGAGCAATCCAGATCGAAATCTACGGT 242
QY 4471 CGTGGTCTCGACTGATACTACTAGTACTTTCATCCTTACTTCTCGCCCAAGTTACTC 4530
DB 243 CGTGGTCTCGACTGATACTACTAGTACTTTCATCCTTACTTCTCGCCCAAGTTACTC 302
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DB 303 AAACCCCTAGCAAGTCTCATAGCTACGGTCAAAATCCCGGAGTTTAATTCACACTTGGCCAT 362
QY 4591 CTTGCTCTCTCCAAAGCCTTGGAGATTACAAATTCACGACACCTGGATTAGATTGG 4650

DB 363 CTTGCTCTCTCTCCAAAGCCTTGGAGATTACAAATTCACGACCACTGGATTAGATTGG 422
QY 4651 TGGAACTCAATAAGCAACATGATAAGTGG 4680
DB 423 TGGAACTCATATACGCAACATGATACGTGG 452
RESULT 14
B97814 433 bp DNA linear GSS 31-MAR-1998
LOCUS F18P18TFB IGF Arabidopsis thaliana genomic clone F18P18, genomic
DEFINITION survey sequence.
ACCESSION B97814
VERSION B97814.1 GI:2999893
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 433)
AUTHORS Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Linher, K., and
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Adams, M.D. and
Venter, J.C.
TITLE A BAC End Sequence Database for Identifying Minimal Overlaps in
Arabidopsis Genomic Sequencing. Update 3
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: F18P18TR
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
High quality sequence stop: 433.
Location/Qualifiers
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/note="Vector: BelobACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
ORIGIN
Query Match 5.7%; Score 431.4; DB 9; Length 433;
Best Local Similarity 99.8%; Pred. No. 2.5e-66;
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DB 1 CTCATTTCTTGGAGACCCATTATGAGACATTTGAGACATCTATAGCAATATATGTAATG 60
QY 5519 TATATTAACGTACTTAAAGTGAATTTTATGACCAAGTAAATAAATATATGCCGAATGTA 5578
DB 61 TATATTAACGTACTTAAAGTGAATTTTATGACCAAGTAAATAAATATATGCCGAATGTA 120
QY 5579 CATGTAATATCGAGTTTAAACTATTTTTCGAATATATAACAATTTTCTCTTCGTC 5638
DB 121 CATGTAATATCGAGTTTAAACTATTTTTCGAATATATAACAATTTTCTCTTCGTC 180
QY 5639 AACTTATATATCTTATTTCTGATTTTCTCTTTTAAATTCCTTTTCCCTTCC 5698
DB 181 AACTTATATATCTTATTTCTGATTTTCTCTTTTAAATTCCTTTTCCCTTCC 240
QY 5699 AAGACACAAAAAATAACAGAAACGAAAAAGAGATTTTAAATAATTCATAACCC 5758

Db 241 AAGACACAAAAAATAACAGAACAAAAAGAGATTTTAAAAATTCATAACCC 300
QY 5759 ACGAGAAATATGACCTAAATTCAGACTAATCCCCAAATTTTCAGAAATTTATGTATTTT 5818
Db 301 ACGAGAAATATGACCTAAATTCAGACTAATCCCCAAATTTTCAGAAATTTATGTATTTT 360
QY 5819 TCGGATTTAAATTTGTTTCAATCAATGCGCACTAATTAATTAAGAAAGACAATGG 5878
Db 361 TCGGATTTAAATTTGTTTCAATCAATGCGCACTAATTAATTAAGAAAGACAATGG 420
QY 5879 AATGACTGAAACC 5891
Db 421 AATGACTGAAACC 433

RESULT 15

CL517384
LOCUS CL517384 468 bp DNA linear GSS 02-APR-2004
DEFINITION SAG3B03 Flanking Sequence Tag of Oryza sativa T-DNA insertion lines
Oryza sativa (japonica cultivar-group) genomic, genomic survey
sequence.

ACCESSION CL517384
VERSION CL517384.1 GI:46144159

KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoideae; Oryza.

REFERENCE 1 (bases 1 to 468)
AUTHORS Sallaud, C., Gay, C., Larmande, P., Bes, M., Piffanelli, P., Piegou, B.,
Droc, G., Regad, F., Bourgeois, E., Meynard, D., Perin, C.,
Ghesquiere, A., Delseny, M., Glaszmann, J.C. and Guiderdoni, E.
TITLE High throughput T-DNA insertion mutagenesis in rice: A first step
towards in silico reverse genetics
JOURNAL Plant J. (2004) In press
COMMENT Contact: Guiderdoni
UMR PIA Biotrop program
CIRAD

TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE

Tel: 33467615629

Fax: 33467615605

Email: emmanuel.guiderdoni@cirad.fr

Class: TDNA tagged.

Location/Qualifiers

1. 468
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="Genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone_lib="Flanking Sequence Tag of Oryza sativa T-DNA
insertion lines"
/note="PCR was performed on DNA of primary transformants
of Oryza sativa plants. The DNA fragment(s) resulting of
PCR were directly sequenced from the left border to
determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed. Information to order
the corresponding mutant line and a link to a database
providing a graphical display is available from June 2004
at <http://genoplante-info.infobiogen.fr/oryzatagline/>.
This sequence has been generated in the framework of the
French plant genomics program Genoplante
(<http://www.genoplante.org> and
<http://genoplante-info.infobiogen.fr>).

ORIGIN

Query Match 5.6%; Score 424.8; DB 10; Length 468;
Best Local Similarity 94.6%; Pred. No. 3.8e-65;
Matches 456; Conservative 0; Mismatches 12; Indels 14; Gaps 1;
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QY 6359 TGGATCCGAGAGGTTTCCCGATATTACCTTTTGTGAAAAAGTCTCAATAGCCCTCTGG 6458
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QY 6579 TTTTCCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTTGGGACCACTCTCGTAGAGGCA 6638
Db 287 TTTTCCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTTGGGACCACTCTCGTAGAGGCA 346
QY 6639 TCTTGAACGATAGGCTTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTCTTT 6698
Db 347 TCTTGAACGATAGGCTTTTCTTTATCGCAATGATGGCAATTTGTAGGTGCCACCTTCTCTTT 406
QY 6699 TCTACTGTCTTTTCGATGAAGTGAAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCC 6758
Db 407 TCTACTGTCTTTTGTATGAAGTGAAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCC 466
QY 6759 GA 6760
Db 467 GA 468

Search completed: December 31, 2005, 05:09:55

Job time : 17838 secs

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OM nucleic - nucleic search, using sw model

Run on: December 30, 2005, 15:08:00 ; Search time 24337 Seconds
(without alignments)
17704.457 Million cell updates/sec

Title: US-10-650-249-1

Perfect score: 7580

Sequence: 1 agctctattaatcaagaga.....gccgcaccgcggtgagct 7580

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_ste.*

11: gb_sv.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6131.2	80.9	103240	15	ATT22E16
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c	3	1402.4	18.5	10450	11 AF218466
4	1163	15.3	1457	15	AK221402
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c	7	640.2	8.4	12537	11 AY788908
c	8	640.2	8.4	12607	11 AY737283
c	9	621	8.2	5033	6 I28266
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11	617.2	8.1	8731	11	CVU10491
12	617.2	8.1	8742	11	AF234315
13	617.2	8.1	8894	11	AF234313
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20	617.2	8.1	9182	11	AF294978	AF294978 Cloning v
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24	617.2	8.1	11633	11	AF234316	AF234316 Binary ve
c	25	617.2	8.1	11667	6	AX840053 Sequence
26	617.2	8.1	11785	11	AF234314	AF234314 Binary ve
27	617.2	8.1	11846	11	AF354045	AF354045 Binary ve
28	617.2	8.1	11849	11	AF234297	AF234297 Binary ve
29	617.2	8.1	11881	11	AY739899	AY739899 Cloning v
30	617.2	8.1	11921	11	AF354046	AF354046 Binary ve
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41	616.8	8.1	8909	11	CVU10458	U10458 Binary clon
42	616.8	8.1	9014	11	CVU10462	U10462 Binary clon
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44	616.8	8.1	12607	11	AY737283	AY737283 C-termina
45	616.6	8.1	8860	11	AF234301	AF234301 Binary ve

ALIGNMENTS

ATT22E16 103240 bp DNA linear PLN 16-APR-2005
Arabidopsis thaliana DNA chromosome 3, BAC clone T22E16.

AL132975.1 GI:6434228

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

misc_feature

gene

CDS

Location/Qualifiers

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QY	1621	TGTTGTGACATAGTAGGTTCCATTTAAAGAAGGTCTGATTTAAATTTTACGTTTGGAC	1680	
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QY	1681	CACAAATCTTTCTTTTAGAAATCGGGACTGGGACCTTCTTACCAACATGTCCTGCTTT	1740	
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RESULT 2

AF187951/c

LOCUS

DEFINITION

ACCESSION

AF187951 10138 bp DNA linear SYN 11-MAY-2000

Activation-tagging vector pSK1015, complete sequence.

AF187951

VERSION	AF187951.1	GI:6537289	
KEYWORDS	Activation-tagging vector pSKI015		
SOURCE	Activation-tagging vector pSKI015		
ORGANISM	other sequences; artificial sequences; vectors.		
REFERENCE	1 (bases 1 to 10138)		
AUTHORS	Weigel,D., Ahn,J.H., Blazquez,M.A., Borevitz,J.O., Kardailsky,I., Christensen,S.K., Fankhauser,C., Ferrandiz,C., Kardailsky,I., Malancharuvill,E.J., Neff,M.M., Nguyen,J.F., Sato,S., Wang,Z., Xia,Y., Dixon,R.A., Harrison,M.J., Lamb,C.J., Yanofsky,M.F. and Chory,J.		
TITLE	Activation tagging in Arabidopsis		
JOURNAL	Plant Physiol. 122 (4), 1003-1013 (2000)		
PUBMED	10759496		
REFERENCE	2 (bases 1 to 10138)		
AUTHORS	Kardailsky,I. and Weigel,D.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-SEP-1999) Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
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	/note="T-DNA left border"		
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Db 2881 AGCGGCCGCCACCGGCTGGAGCT 2858

RESULT 3
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DEFINITION Activation tagging vector pSKI074, complete sequence.
ACCESSION AF218466
VERSION AF218466.1 GI:6715465
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Weigel,D., Ahn,J.H., Blazquez,M.A., Borevitz,J.O.,
Christensen,S.K., Fankhauser,C., Ferrandiz,C., Kardailsky,I.,
Malancharuvil,E.J., Neff,M.M., Nguyen,J.T., Sato,S., Wang,Z.,
Xia,Y., Dixon,R.A., Harrison,M.J., Lamb,C.J., Yanofsky,M.F. and
Chory,J.
TITLE Activation tagging in Arabidopsis
JOURNAL Plant Physiol. 122 (4), 1003-1013 (2000)
PUBMED 10759496
REFERENCE 2 (bases 1 to 10450)
AUTHORS Weigel,D., Blazquez,M.A., Borevitz,J., Christensen,S.K.,
Fankhauser,C., Ferrandiz,C., Malancharuvil,E.J., Neff,M.M.,
Nguyen,J.T., Sato,S., Xia,Y., Wang,Z., Dixon,R.A., Harrison,M.J.,
Lamb,C.J., Yanofsky,M.F. and Chory,J.
Direct Submission
Submitted (22-DEC-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA
FEATURES
Location/Qualifiers
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Query Match 18.5%; Score 1402.4; DB 11; Length 10450;
Best Local Similarity 99.9%; Pred. No. 1.7e-195;
Matches 1403; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	2881	AGCGGCGCCACCGCGGTGGAGCT	2858
RESULT 4			
AK221402			
LOCUS			
DEFINITION	Arabidopsis thaliana gene for zinc finger protein OBP3, complete cds, clone: RAFL25-48-C17.		
ACCESSION	AK221402		
VERSION	AK221402.1 GI:62320151		
KEYWORDS	FLI CDNA.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K., Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K., Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.		
TITLE	Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1457)		
AUTHORS	Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K., Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K., Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-MAR-2005) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:mseki@gsc.riken.jp.		
	URL:http://rarge.gsc.riken.jp/, Tel:81-45-503-9625,		

Fax:81-45-503-9586)
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145).
This clone is in a modified pBluescript vector.
Please visit our web site (<http://rarge.gsc.riken.jp/>) for further details.

Location/Qualifiers
1. 1457
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/mol_type="mRNA"
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/chromosome="3"
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/ecotype="Columbia"
/note="common name: thale cress"
1. 1457
/gene="At3g55370"
134. 1105
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/protein_id="BAD94355.1"
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PSKPHSYQOIPEFNSNLPILPLOSGLDYSNLTGLDFGGTQISNMISSMSSGGILD
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ORIGIN

Query, Match	15.3%;	Score 1163;	DB 15;	Length 1457;
Best Local Similarity	93.2%;	Pred. No. 2.9e-160;		
Matches 1266;	Conservative 0;	Mismatches 0;	Indels 93;	Gaps 1;

QY 4105 GCAGCAAGGGAACCAACATCAGCTAGAATGTGTCAACCTGACCAAGACCCCTAATAATTA 4164
Db 184 GCAGCAAGGGAACCAACATCAGCTAGAATGTGTCAACCTGACCAAGACCCCTAATAATTA 243
QY 4165 TTACGGCAGCTCTCATCAACCACTTCTCAGGTTGAGGTTGAGTCAAGCTAGAGT 4224
Db 244 TTACGGCAGCTCTCATCAACCACTTCTCAGGTTGAGGTTGAGTCAAGCTAGAGT 303
QY 4225 GAATTCATGTTGGAGAGCTGCTCGATCGCAAAAGTCCCATTCCTGAGAGAGCTCTAAA 4284
Db 304 GAATTCATGTTGGAGAGCTGCTCGATCGCAAAAGTCCCATTCCTGAGAGAGCTCTAAA 363
QY 4285 TTGCCCTAGATGTGACTCAACCAATACTAAAGTTCTGTACTTCAATAACTATAGCCTTAC 4344
Db 364 TTGCCCTAGATGTGACTCAACCAATACTAAAGTTCTGTACTTCAATAACTATAGCCTTAC 423
QY 4345 TCAACTCGCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTTGGGGGTTCTTGGAG 4404
Db 424 TCAACTCGCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTTGGGGGTTCTTGGAG 483
QY 4405 GAATGTTCTGTTGGAGAGGCTTTAGGAGGAACAGAGAAGCAATCCAGATCGAAATC 4464
Db 484 GAATGTTCTGTTGGAGAGGCTTTAGGAGGAACAGAGAAGCAATCCAGATCGAAATC 543
QY 4465 TACGGTCTGGTCTCGACTGATACTACTAGTACTTCACTCACTTCTTCTCGCCCAAG 4524
Db 544 TACGGTCTGGTCTCGACTGATACTACTAGTACTTCACTCACTTCTTCTCGCCCAAG 603
QY 4525 TTACTCAAAACCTTAGCAAGTTTCATAGCTACGGTCAAAATCCCGGAGTTTAAATCCAACTT 4584
Db 604 TTACTCAAAACCTTAGCAAGTTTCATAGCTACGGTCAAAATCCCGGAGTTTAAATCCAACTT 663
QY 4585 GCCCATCTTGCTCTCTCCAAAGCTTGGAGATTACAAATTCAGCAACACACTGGATTAGA 4644
Db 664 GCCCATCTTGCTCTCTCCAAAGCTTGGAGATTACAAATTCAGCAACACACTGGATTAGA 723
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[illegible]

RESULT 5					
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LOCUS	AF155818	1274 bp	mRNA	linear	PLN 23-DEC-1999
DEFINITION	Arabidopsis thaliana zinc finger protein OBP3 mRNA, complete cds.				

KEYWORDS	Arabidopsis thaliana (thale cress)
SOURCE	Arabidopsis thaliana
ORGANISM	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
	rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1 (Bases 1 to 1274);
AUTHORS	Kang, H. G. and Singh, K. B.
TITLE	Characterization of Arabidopsis Dof Transcription Factors, a Novel
	Zinc Finger Protein Family in Plants
JOURNAL	Unpublished

REFERENCE	2	(bases 1 to 1274)
AUTHORS	Kang,H.G. and Singh,K.B.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-JUN-1999) MCD8, University of California, Los Angeles, 405 Hilgard Ave., Los Angeles, CA 90095, USA	
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source	1..1274	
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Best local Similarity	92.9%; Pred. No. 2.9e-159;	
Matches 1261; Conservative	0; Mismatches 3; Indels 93; Gaps 1;	
QY	4105 GCAGCAGGGAACCAACATCAGCTAGAACTGTGCACAACCTGACCAGAACCTTAATAATTA 4164	
DB	11 GGAGTAAGGAAACACATCAGCTAGNATGTGCACAACTGACCAAGCAACCTTAATAATTA 70	
QY	4165 CTTACGCGAGCTCTCATACCACCGACTTCTCAGGTTGCAAGTTGCGAGTCAAGCTAGAGT 4224	
DB	71 CTTAGGCGAGCTCTCATACCACCGACTTCTCAGGTTGCAAGTTGCGAGTCAAGCTAGAGT 130	
QY	4225 GAATTCATAGTGGAGCGTGCTCGATCGCAAAAGTCCATTCGCTCAAGCAGCTCTAAA 4284	
DB	131 GAATTCAAATGGTGGAGCGTGCTCGGATCGCAAAAGTCCCATTCGCTCAAGCAGCTCTAAA 190	
QY	4285 TTGCGCTAGATGTGACTCAACCAATACTAAGTTCTGTGTACTTCAATAACTATAGCCCTTAC 4344	
DB	191 TTGCGCTAGATGTGACTCAACCAATACTAAGTTCTGTGTACTTCAATAACTATAGCCCTTAC 250	
QY	4345 TCAACCTCGGCATTTCTTGCAAAACATGTCGCTCGCTATTTGGACACGTCGGCGGTTCTCTTGAG 4404	
DB	251 TCAACCTCGGCATTTCTTGCAAAACATGTCGCTCGCTATTTGGACACGTCGGCGGTTCTCTTGAG 310	
QY	4405 GAATGTTCTGTTGGAGGAGGCTTTAGGAGGAACAAGAGAAACAAATCCAGATCGAAATC 4464	
DB	311 GAATGTTCTGTTGGAGGAGGCTTTAGGAGGAAACAAGAGAAACAAATCCAGATCGAAATC 370	
QY	4465 TAGGTCGTGGTCTCGACTGATAATACTACTAGTACTTCACTTCACTTACTTCTCGCCCCAAG 4524	
DB	371 TAGGTCGTGGTCTCGACTGATAATACTACTAGTACTTCACTTCACTTACTTCTCGCCCCAAG 430	
QY	4525 TTACTCAAAACCTTAGCAAGTTTTCATAGTACGGTCAAATCCCCGGAGTTTAATTCCAACTT 4584	
DB	431 TTACTCAAAACCTTAGCAAGTTTTCATAGTACGGTCAAATCCCCGGAGTTTAATTCCAACTT 490	
QY	4585 GCCCATCTTGCCTCCTCTCCAAAGCCCTTGAGATTTACAATTCAAAGCAACACTGTGATTAGA 4644	
DB	491 GCCCATCTTGCCTCCTCTCCAAAGCCCTTGAGATTTACAATTCAAAGCAACACTGTGATTAGA 550	
QY	4645 TTTTGTGGAACTCAAAATAGCAACATGATAAGTGGTATGAGTTCTAGTCGTGGGATCTT 4704	
DB	551 TTTTGTGGAACTCAAAATAGCAACATGATAAGTGGTATGAGTTCTAGTCGTGGGATCTT 610	
QY	4705 GGATGCATGAGAAATACCTCCATCAACAACAGCTCAGCAATTCCTCTTCTTGTGATCAACAC 4764	
DB	611 GGATGCATGAGAAATACCTCCATCAACAACAGCTCAGCAATTCCTCTTCTTGTGATCAACAC 670	
QY	4765 TACCGGATTCGGTGCATTTCTCAACACCGGTTATATCCATTAATAGAAAGGTAAGGAGGTGT 4824	

Db 671 TACCGGATGGTGCATCTTCAACGCGGTATATCATCTACTAGA----- 715
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Db 716 ----- 715
QY 4885 CTTGATGGATTTTCTTACGGCGGGTTAGCCCGACGCAACAAAGAAATGTGAAGCGGA 4944
Db 716 -----AGCGGGGTTAGCCCGACGCAACAAAGAAATGTGAAGCGGA 757
QY 4945 AGAGAATGATCAGGATCGGGGTAGGATCGGGATCGAGTGAATACTTATCAAGAAACTT 5004
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QY 5005 TTTGGGTAAATCAACATAAACTCAGGCAGGACGAGGAATACATCATGCGGAGGTAA 5064
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Db 938 CAGCACTAGCTATCTTGAATGATCTTTTGTGGTGTACATGCTGTGTCAT 997
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QY 5365 ATATTGGCTATATAGAGGTGTGGGTGATATGATGAATTCAGAGTTGATGTTGGAAA 5424
Db 1178 ATATTGGCTATATAGAGGTGTGGGTGATATGATGAATTCAGAGTTGATGTTGGAAA 1237
QY 5425 CTTTGTGTGTTCAATGAATAATCATCGAATTC 5461
Db 1238 CTTTGTGTGTTCAATGAATAATCATCGAATTC 1274

RESULT 6
AF406991/c
LOCUS
DEFINITION
Tobacco rattle virus RNA2-based VIGS vector pTRV2, complete
ACCESSION
AF406991
VERSION
AF406991.1 GI:21389151
KEYWORDS
Tobacco rattle virus RNA2-based VIGS vector pTRV2 (pYL156)
SOURCE
Tobacco rattle virus RNA2-based VIGS vector pTRV2
ORGANISM
other sequences; artificial sequences; vectors.
REFERENCE
1 (bases 1 to 9663)
AUTHORS
Liu,Y., Schiff,M., Marathe,R. and Dinesh-Kumar,S.P.
TITLE
Tobacco Rar1, EDS1 and NPR1/NIM1 like genes are required for
N-mediated resistance to tobacco mosaic virus
JOURNAL
Plant J. 30 (4), 415-429 (2002)
PUBMED
12028572
REFERENCE
2 (bases 1 to 9663)
AUTHORS
Liu,Y.
TITLE
Direct Submission
SUBMITTED (08-AUG-2001) MCDB, Yale University, 165 Prospect Street,
New Haven, CT 06520, USA
JOURNAL
Location/Qualifiers
FEATURES
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source
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pTRV2 "
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/db_xref="taxon:188057"
/note="Tobacco rattle virus RNA2-based T-DNA vector
synonym: pYL156"
1..1639
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1640..1708
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1709..2103
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2104..2154
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2155..8894
misc_feature
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8895..9663
promoter
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ORIGIN

Query Match 8.4%; Score 640.2; DB 11; Length 9663;
Best Local Similarity 98.4%; Pred. No. 3.9e-84;
Matches 660; Conservative 0; Mismatches 3; Indels 8; Gaps 1;
QY 6190 AGATATCATCAATCACTTCTTGAAGACGTGGTTGGAACGCTCTTTTTCACGA 6249
Db 9577 AGATATCATCAATCACTTCTTGAAGACGTGGTTGGAACGCTCTTTTTCACGA 9518
QY 6250 TGTTCCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 6309
Db 9517 TGTTCCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 9458
QY 6310 TAGCCTTTCCTTATCGCAATGATGGCATTTGTAGAAGCATCTTCTTTTCTACTGTCC 6369
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QY 6370 TTTTCGATCAAGTGA CAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 6429
Db 9397 TTTTCGATCAAGTGA CAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 9338
QY 6430 TTTTGTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGG 6489
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QY 6490 AGTAGACGAGAGTGTCTGAGTCCACCATGTTGGGGATCTAGATATCAATCAATCCACTT 6549
Db 9277 AGTAGACGAGAGTGTCTGAGTCCACCATGTTG-----ACCATCAATCAATCCACTT 9226
QY 6550 GCTTTGAAAGACGTGGTTGGAACGCTCTTCTTTTCCACGATGTTCTCGTGGGTGGGGTTC 6609
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QY 6610 CATCTTTGGACCACTGTGCGTAGAGGCATCTTGAACGATGACCTTTCTTTTATCGCAAT 6669
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QY 6670 GATGCAATTTGAGAGGCATCTTCTTTTCTACTGTCTTTTCGATGAAGTGCACAGATAG 6729
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QY 6730 CTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCTTTTGTGAAAAGTCTCAATAG 6789
Db 9045 CTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCTTTTGTGAAAAGTCTCAATAG 8986
QY 6790 CCTCTGTGCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGTGTCTGTGCT 6849
Db 8985 CCTCTGTGCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGTGTCTGTGCT 8926
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Db 8925 CCACCATGTTG 8915

RESULT 7

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LOCUS AY788908 12537 bp DNA circular SYN 02-MAR-2005
DEFINITION N-terminal TAPA T-DNA vector pN-TAPA, complete sequence.
ACCESSION AY788908
VERSION AY788908.1 GI:55824365
KEYWORDS N-terminal TAPA T-DNA vector pN-TAPA
SOURCE N-terminal TAPA T-DNA vector pN-TAPA
ORGANISM N-terminal TAPA T-DNA vector pN-TAPA
REFERENCE 1 (bases 1 to 12537)
AUTHORS Rubio,V., Shen,Y., Saijo,Y., Liu,Y., Gusmaroli,G.,
Dinesh-Kumar,S.P., and Deng,X.W.
TITLE An alternative tandem affinity purification strategy applied to
Arabidopsis protein complex isolation
JOURNAL Plant J. 41 (5), 767-778 (2005)
PUBMED 15703063
REFERENCE 2 (bases 1 to 12537)
AUTHORS Rubio,V. and Deng,X.W.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (21-OCT-2004) MCDB, Yale University, 165, Prospect St.,
New Haven, CT 06511, USA
FEATURES
Location/Qualifiers
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Query Match 8.4%; Score 640.2; DB 11; Length 12537;
Best Local Similarity 98.4%; Pred. No. 3.6e-84;
Matches 660; Conservative 0; Mismatches 3; Indels 8; Gaps 1;
QY 6190 AGATATCATCAATCAATCCACTGCTTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 6249
DB 683 AGATATCATCAATCAATCCACTGCTTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 624
QY 6250 TGTTCTCGTGGGTGGGTCATCTTTGGGACCACTGTCGGTAGAGGCATCTTCCGATATACCC 6309
DB 623 TGTTCTCGTGGGTGGGTCATCTTTGGGACCACTGTCGGTAGAGGCATCTTCCGATATACCC 564
QY 6310 TAGCCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTCC 6369
DB 563 TAGCCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTCC 504
QY 6370 TTTCGATGAAGTAGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATATACC 6429
DB 503 TTTCGATGAAGTAGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATATACC 444
QY 6430 TTGTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTGATATCTTGG 6489
DB 443 TTGTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTGATATCTTGG 384
QY 6490 ACTAGACGAGAGTGTGCTGCCACCATGTTTGGGATCTAGATATCAATCAATCACTT 6549
DB 383 AGTAGACGAGAGTGTGCTGCCACCATGTTTGGGATCTAGATATCAATCAATCACTT 332

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QY 6550 GCTTTGAAGACGTGCTTGGAAAGCTCTTCTTTTCCACGATGTTCTCGTGGGTGGGGTC 6609
DB 331 GCTTTGAAGACGTGCTTGGAAAGCTCTTCTTTTCCACGATGTTCTCGTGGGTGGGGTC 272
QY 6610 CATCTTTGGGACCACTGTCGGTAGAGGCATCTTTGAACGATAGCCCTTTCTTTATCGCAAT 6669
DB 271 CATCTTTGGGACCACTGTCGGTAGAGGCATCTTTGAACGATAGCCCTTTCTTTATCGCAAT 212
QY 6670 GATGCATTTGTAGAAGCACTCTTCTTTTCTACTGTCTTTCGATGAAGTGCACAGATAG 6729
DB 211 GATGCATTTGTAGAAGCACTCTTCTTTTCTACTGTCTTTCGATGAAGTGCACAGATAG 152
QY 6730 CTGGCAATGGAATCCGAGGAGGTTTCCGATATATACCTTTGTGAAAAGTCTCAATAG 6789
DB 151 CTGGCAATGGAATCCGAGGAGGTTTCCGATATATACCTTTGTGAAAAGTCTCAATAG 92
QY 6790 CCCTCTGCTCTTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAGTGTCTGCT 6849
DB 91 CCCTCTGCTCTTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAGTGTCTGCT 32
QY 6850 CCACCATGTTG 6860
DB 31 CCACCATGTTG 21
RESULT 8
AY737283/c
LOCUS AY737283 12607 bp DNA circular SYN 02-MAR-2005
DEFINITION C-terminal TAP T-DNA vector pYL436, complete sequence.
ACCESSION AY737283
VERSION AY737283.1 GI:52630860
KEYWORDS C-terminal TAP T-DNA vector pYL436
ORGANISM C-terminal TAP T-DNA vector pYL436
REFERENCE 1 (bases 1 to 12607)
AUTHORS Rubio,V., Shen,Y., Saijo,Y., Liu,Y., Gusmaroli,G.,
Dinesh-Kumar,S.P., and Deng,X.W.
TITLE An alternative tandem affinity purification strategy applied to
Arabidopsis protein complex isolation
JOURNAL Plant J. 41 (5), 767-778 (2005)
PUBMED 15703063
REFERENCE 2 (bases 1 to 12607)
AUTHORS Liu,Y. and Dinesh-Kumar,S.P.
TITLE A C-terminal tandem affinity purification (TAP) T-DNA vector pYL436
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 12607)
AUTHORS Liu,Y. and Dinesh-Kumar,S.P.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-2004) MCDB, Yale University, New Haven, CT 06520,
USA
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/note="NOS terminator"

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Query Match 8.4%; Score 640.2; DB 11; Length 12607; Best Local Similarity 98.4%; Pred. No. 3.6e-84; Matches 660; Conservative 0; Mismatches 3; Indels 8; Gaps 1;		Query Match 8.2%; Score 621; DB 6; Length 5033; Best Local Similarity 95.1%; Pred. No. 3e-81; Matches 653; Conservative 0; Mismatches 30; Indels 4; Gaps 1;	
QY 6190	AGATATCACATCAATCCACTTGTGAGAGCGTGTGGAAACGTCCTTTTCCACGA 6249	QY 6868	AGATATCACATCAATCCACTTGTGAGAGCGTGTGGAAACGTCCTTTTCCACGA 6927
DB 683	AGATATCACATCAATCCACTTGTGAGAGCGTGTGGAAACGTCCTTTTCCACGA 624	DB 1103	AGATATCACATCAATCCACTTGTGAGAGCGTGTGGAAACGTCCTTTTCCACGA 1044
QY 6250	TGTTCTCGTGGGTCCATCTTTGGGACCACTGTCGTAGAGGCATCTTGAACGA 6309	QY 6928	TGTTCTCGTGGGTCCATCTTTGGGACCACTGTCGTAGAGGCATCTTGAACGA 6987
DB 623	TGTTCTCGTGGGTCCATCTTTGGGACCACTGTCGTAGAGGCATCTTGAACGA 564	DB 1043	TGTTCTCGTGGGTCCATCTTTGGGACCACTGTCGTAGAGGCATCTTGAACGA 984
QY 6310	TAGCCCTTTCCTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTACTGTCC 6369	QY 6988	TAGCCCTTTCCTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTACTGTCC 7047
DB 563	TAGCCCTTTCCTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTACTGTCC 504	DB 983	TAGCCCTTTCCTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTACTGTCC 924
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DB 503	TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACC 444	DB 923	TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACC 864
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LOCUS I28266/c		LOCUS CVU10488	
DEFINITION Sequence 1 from patent US 5569828.		DEFINITION Binary cloning vector pPZP121 for plant transformation, complete sequence.	
ACCESSION I28266		ACCESSION U10488	
VERSION I28266.1		VERSION U10488.1	
KEYWORDS GI:1919042		KEYWORDS GI:506683	
SOURCE Unknown.		SOURCE Cloning vector pPZP121	
ORGANISM Unknown.		ORGANISM Cloning vector pPZP121	
REFERENCE 1 (bases 1 to 5033)		REFERENCE 1 (bases 1 to 8626)	
AUTHORS McMullen,M.D.; Koch,B.A. and Townsend,R.		AUTHORS Hajdukiewicz,P.; Svab,Z. and Maliga,P.	
TITLE Maize chlorotic dwarf virus and resistance thereto		TITLE The small, versatile pp2p family of Agrobacterium binary vectors for plant transformation	
JOURNAL Patent: US 5569828-A 1 29-OCT-1996;		JOURNAL Plant Mol. Biol. 25 (6), 989-994 (1994)	
FEATURES Location/Qualifiers		PUBMED 7919218	
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AUTHORS Hajdukiewicz, P.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1994) Peter Hajdukiewicz, Waksman Institute,
Rutgers University, Old Hoes Lane, Piscataway, NJ 08855, USA
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Best Local Similarity 93.6%; Pred. No. 9.2e-81;
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QY 6928 TGTTCCTCGTGGTGGGGTGCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 6987
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DEFINITION Binary cloning vector pPZP221 for plant transformation, complete
sequence.
ACCESSION U10491
VERSION U10491.1 GI:506686
KEYWORDS
SOURCE Cloning vector pPZP221

ORGANISM Cloning vector pPZP221
REFERENCE 1 (bases 1 to 8731)
AUTHORS Hajdukiewicz, P., Svab, Z. and Maliga, P.
TITLE The small, versatile pPZP family of Agrobacterium binary vectors
for plant transformation
JOURNAL Plant Mol. Biol. 25 (6), 989-994 (1994)
PUBMED 7919218
REFERENCE 2 (bases 1 to 8731)
AUTHORS Hajdukiewicz, P.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1994) Peter Hajdukiewicz, Waksman Institute,
Rutgers University, Old Hoes Lane, Piscataway, NJ 08855, USA
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ORGANISM		SOURCE	Binary vector pCambia-2300			
REFERENCE		1 (sites)	other sequences; artificial sequences; vectors.			
AUTHORS		Hajdukiewicz, P., Svab, Z. and Maliga, P.				
TITLE		The small, versatile pP2P family of Agrobacterium binary vectors for plant transformation				
JOURNAL		Plant Mol. Biol. 25 (6), 989-994 (1994)				
PUBMED		7919218				
REFERENCE		2 (bases 1 to 8742)				
AUTHORS		Roberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W., Nugrohu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L., Svab, Z., Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.				
TITLE		A comprehensive set of modular vectors for advanced manipulations and efficient transformation of plants				
JOURNAL		Unpublished				
REMARK		Full description of constructs				
REFERENCE		3 (bases 1 to 8742)				
AUTHORS		Roberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W., Nugrohu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L., Svab, Z., Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.				
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VERSION AF234313.1
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ORGANISM Binary vector pCambia-2200
OTHER SEQUENCES; artificial sequences; vectors.
REFERENCE 1 (sites)
AUTHORS Hajdukiewicz, P., Svab, Z., and Maliga, P.
TITLES The small, versatile pP2P family of Agrobacterium binary vectors for plant transformation
JOURNAL Plant Mol. Biol. 25 (6), 989-994 (1994)
PUBMED 7913218
REFERENCE 2 (bases 1 to 8894)
AUTHORS Roberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W., Nugrohu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L., Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z., Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.
TITLES A comprehensive set of modular vectors for advanced manipulations and efficient transformation of plants
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 8894)
AUTHORS Roberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W., Nugrohu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L., Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z., Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.
TITLES Direct Submission
JOURNAL Submitted (15-FEB-2000) CAMBIA, Clunies Ross St, Black Mountain /
GPO Box 3200, Canberra, ACT 2601, Australia
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AUTHORS	Hajdukiewicz, P., Svab, Z. and Maliga, P.		
TITLE	The small, versatile pPZP family of Agrobacterium binary vectors for plant transformation		
JOURNAL	Plant Mol. Biol. 25 (6), 989-994 (1994)		
PUBMED	7919218		
REFERENCE	2 (bases 1 to 8909)		
AUTHORS	Hajdukiewicz, P.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-JUN-1994) Peter Hajdukiewicz, Waksman Institute, Rutgers University, Old Hoes Lane, Piscataway, NJ 08855, USA		
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AUTHORS	Hajdukiewicz, P., Svab, Z. and Maliga, P.		
TITLE	The small, versatile pPZP family of Agrobacterium binary vectors for plant transformation		
JOURNAL	Plant Mol. Biol. 25 (6), 989-994 (1994)		
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AUTHORS	Roberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W., Nugrohu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L., Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z., Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.		
TITLE	A comprehensive set of modular vectors for advanced manipulations and efficient transformation of plants		
JOURNAL	Unpublished		
REMARK	Full description of constructs		
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AUTHORS	Roberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W., Nugrohu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L., Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z., Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.		
TITLE	Direct Submission		
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7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7580	100.0	7580	12	ADL71829 Arabidops
2	1503	19.8	1746	12	ADL71846 Arabidops
3	1402	18.5	10078	6	ABQ73047 Tomato an
4	1367	18.0	17511	14	ADV39061 Plant gen
5	1367	18.0	18987	14	ADV39062 Plant gen
6	1360	17.9	1361	3	AAa88401 4X CamV 3
7	1235	16.3	1235	12	ADL71845 Arabidops
8	1052	14.0	1052	12	ADL71848 Arabidops
9	1058	14.0	1058	12	ADL71847 Arabidops
10	888	11.7	888	12	ADL71840 Arabidops
11	684	9.0	684	12	ADL71843 Arabidops
12	581	7.7	645	10	ADK59804 Plant DNA
13	581	7.7	795	10	ADD30377 Plant yie
14	581	7.7	795	12	ADI44304 Plant tra
15	577	7.6	577	10	ABX56844 Arabidops
16	368	4.9	2000	6	AB215758 Arabidops
17	331	4.4	12739	14	ADW39084 Binary ve
18	300	4.0	552	6	AAD39450 FMV35S46
19	299	3.9	323	3	AAC87191 CamV35S p

ALIGNMENTS

RESULT 1

ADL71829

ID ADL71829 standard; DNA; 7580 BP.

XX ADL71829;

XX 20-MAY-2004 (first entry)

XX Arabidopsis thaliana OBP3 DNA.

XX Transgenic plant; Dof transcription factor; ocs binding factor;
KW plant size; plant stature; root growth; plant; gene; db; OBF;
KW OBF binding protein; OBP3; SOB1; mouse-ear cross.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

FT CDS 4103..5119

FT /*tag= a

FT /product= "Arabidopsis thaliana OBP3 protein"

FT /transl_except= (pos:4811..4909, aa:Gly-Gly)

XX US2004045055-A1.

XX 04-MAR-2004.

XX 28-AUG-2003; 2003US-00650249.

XX 28-AUG-2002; 2002US-0406657P.

XX (UNIW) UNIV WASHINGTON.

XX Neff MM;

XX WPI; 2004-225757/21.

XX P-PSDB; ADL71830.

XX New transgenic plant cell, useful in producing plants with altered size
and stature and with normal and healthy root growth.

XX Claim 24; SEQ ID NO 1; 53pp; English.

XX

CC	The invention relates to a transgenic plant transformed by a Dof									
CC	transcription factor, OBP (ocs binding factor) binding protein (OBP3).									
CC	OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic									
CC	acid and polypeptides are useful in producing transgenic plants with									
CC	altered size and stature and with normal and healthy root growth. The									
CC	present sequence is Arabidopsis thaliana OBP3 DNA.									
XX										
SQ	Sequence 7580 BP; 2376 A; 1376 C; 1291 G; 2537 T; 0 U; 0 Other;									
	Query Match	100.0%;	Score 7580;	DB 12;	Length 7580;					
	Best Local Similarity	100.0%;	Pred. No. 0;							
	Matches 7580;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	1	AGCTCTATTAA	TTCAAGAGAG	CAGCAAA	TAAAGCA	AAAAA	CTCAAA	ACCTAA	AGTTTCTCTGA	60
Db	1	AGCTCTATTAA	TTCAAGAGAG	CAGCAAA	TAAAGCA	AAAAA	CTCAAA	ACCTAA	AGTTTCTCTGA	60
Qy	61	ATATGAAGGG	TTAGATAAT	CAATTC	TCTCA	ACTAGT	TAA	AAAAA	AGTAATAAA	120
Db	61	ATATGAAGGG	TTAGATAAT	CAATTC	TCTCA	ACTAGT	TAA	AAAAA	AGTAATAAA	120
Qy	121	AAAAACAAT	GGATCAAT	TAAAGAC	AGTAGT	TTATGAT	TATAT	TATAT	GGGATCGATTA	180
Db	121	AAAAACAAT	GGATCAAT	TAAAGAC	AGTAGT	TTATGAT	TATAT	TATAT	GGGATCGATTA	180
Qy	181	GTTCACATC	CAAAAGAT	CAAAAT	ATAGCC	GGTAAT	TTGCC	CAAAAT	ACCAAGCGCAAT	240
Db	181	GTTCACATC	CAAAAGAT	CAAAAT	ATAGCC	GGTAAT	TTGCC	CAAAAT	ACCAAGCGCAAT	240
Qy	241	CATCGGATAT	TTCAACAC	CTTAA	TGTCT	CAAT	TACTA	TACTA	CTCTCAATTA	300
Db	241	CATCGGATAT	TTCAACAC	CTTAA	TGTCT	CAAT	TACTA	TACTA	CTCTCAATTA	300
Qy	301	CAAAAGCTAG	CTAGATTT	TCTCA	AGTGAG	CAACAG	CTCTAA	TTCTCT	GAAAAA	360
Db	301	CAAAAGCTAG	CTAGATTT	TCTCA	AGTGAG	CAACAG	CTCTAA	TTCTCT	GAAAAA	360
Qy	361	TTTTCCGAG	TGTAAT	TATCC	AACTCT	ACTTACT	TAC	CAATTT	GAGCATTAAT	420
Db	361	TTTTCCGAG	TGTAAT	TATCC	AACTCT	ACTTACT	TAC	CAATTT	GAGCATTAAT	420
Qy	421	CTGCAACT	TTTAAAC	CAGGTGT	CAAGTGT	CAACAC	CAGATCT	TAGG	GTTAAACAC	480
Db	421	CTGCAACT	TTTAAAC	CAGGTGT	CAAGTGT	CAACAC	CAGATCT	TAGG	GTTAAACAC	480
Qy	481	CTAGTACT	TTAAAT	PAGATTT	ATG	CCCTAT	TTTTC	GACCA	TATATAT	540
Db	481	CTAGTACT	TTAAAT	PAGATTT	ATG	CCCTAT	TTTTC	GACCA	TATATAT	540
Qy	541	TTTCGTG	AAAAA	TGCGCAT	GTTC	TGTTG	GAATCT	AGGAAT	CTTCTT	600
Db	541	TTTCGTG	AAAAA	TGCGCAT	GTTC	TGTTG	GAATCT	AGGAAT	CTTCTT	600
Qy	601	GCATGCA	CGTGTAA	CGATTT	CTCA	ATTGTAT	CTAT	CTCGAT	TTTTCC	660
Db	601	GCATGCA	CGTGTAA	CGATTT	CTCA	ATTGTAT	CTAT	CTCGAT	TTTTCC	660
Qy	661	CTTGAAA	TTTAA	AGATCA	AAAT	TATAT	GAGAAC	ATAT	TGTTG	720
Db	661	CTTGAAA	TTTAA	AGATCA	AAAT	TATAT	GAGAAC	ATAT	TGTTG	720
Qy	721	TATATAG	TGTG	TAGATG	TGAACT	ATG	GATAC	AAAAA	CAATAG	780
Db	721	TATATAG	TGTG	TAGATG	TGAACT	ATG	GATAC	AAAAA	CAATAG	780
Qy	781	AGAAGT	GTGTT	TACAA	CTAT	GAAAT	ATG	GGGCT	CATG	840
Db	781	AGAAGT	GTGTT	TACAA	CTAT	GAAAT	ATG	GGGCT	CATG	840
Qy	841	AAGATTC	CTCTG	ATG	CAAAAT	GTGTT	TACT	TAAT	AAAAA	900
Db	841	AAGATTC	CTCTG	ATG	CAAAAT	GTGTT	TACT	TAAT	AAAAA	900

Qy	901	AGACGAA	TTTTCTTTTAA	ATAAATTTCT	TATA	CAAA	TAA	AGATA	AGT	GC	CT	TTTAAA	960
Db	901	AGACGAA	TTTTCTTTTAA	ATAAATTTCT	TATA	CAAA	TAA	AGATA	AGT	GC	CT	TTTAAA	960
Qy	961	AACATG	CAAAAGA	ATATATAG	ATTAC	GGTAT	CGAT	TTTTCAT	ACAAT	TTTTTAT	TTTTT	1020	
Db	961	AACATG	CAAAAGA	ATATATAG	ATTAC	GGTAT	CGAT	TTTTCAT	ACAAT	TTTTTAT	TTTTT	1020	
Qy	1021	TGAGCT	TGAAGAT	TAAACAT	GACAA	CTGTAT	CGTGT	CTCTCGT	CTAT	TAC	CCCTAGA	1080	
Db	1021	TGAGCT	TGAAGAT	TAAACAT	GACAA	CTGTAT	CGTGT	CTCTCGT	CTAT	TAC	CCCTAGA	1080	
Qy	1081	AGAAGT	GAAACAT	GTAACT	TTAT	TGATAT	TG	CATAC	GGCGAG	CTAG	TTCTTCCCT	1140	
Db	1081	AGAAGT	GAAACAT	GTAACT	TTAT	TGATAT	TG	CATAC	GGCGAG	CTAG	TTCTTCCCT	1140	
Qy	1141	TGCAAT	TAGAT	GAAAGACAT	TAT	CAC	T	CAGGTT	CGCTA	CTT	CGAAGCGCA	1200	
Db	1141	TGCAAT	TAGAT	GAAAGACAT	TAT	CAC	T	CAGGTT	CGCTA	CTT	CGAAGCGCA	1200	
Qy	1201	AAAAAT	CGTTTTAG	CTCTAT	CAT	CTGTCT	TTTTG	AAGAA	AAATAT	CAACAT	TCAAA	1260	
Db	1201	AAAAAT	CGTTTTAG	CTCTAT	CAT	CTGTCT	TTTTG	AAGAA	AAATAT	CAACAT	TCAAA	1260	
Qy	1261	TATACAC	CTCC	CCCAATA	TAT	AAC	CAATAT	TAT	TGGT	TACT	ACGAAAT	1320	
Db	1261	TATACAC	CTCC	CCCAATA	TAT	AAC	CAATAT	TAT	TGGT	TACT	ACGAAAT	1320	
Qy	1321	GATATT	GGCTTTG	AAACAA	CTTAA	ACTGT	GAATTA	CAAG	CTAAG	CAATAT	TATCTAT	1380	
Db	1321	GATATT	GGCTTTG	AAACAA	CTTAA	ACTGT	GAATTA	CAAG	CTAAG	CAATAT	TATCTAT	1380	
Qy	1381	ATTCTTT	CTTTG	TGCTCA	ACTTCA	TCCTTTCT	TAAG	TAAT	TCAA	ATTTAA	TTTGG	1440	
Db	1381	ATTCTTT	CTTTG	TGCTCA	ACTTCA	TCCTTTCT	TAAG	TAAT	TCAA	ATTTAA	TTTGG	1440	
Qy	1441	TGTCAT	CTAAA	TTGAAG	TTTCTT	CTAC	CGGAT	CA	TTTTG	CTCAG	TTTGCATAT	1500	
Db	1441	TGTCAT	CTAAA	TTGAAG	TTTCTT	CTAC	CGGAT	CA	TTTTG	CTCAG	TTTGCATAT	1500	
Qy	1501	CTTAGT	CTGAT	CGAAAA	CTTTATA	ATAAT	TAT	TGATT	AGAGAG	AGACAT	GT	1560	
Db	1501	CTTAGT	CTGAT	CGAAAA	CTTTATA	ATAAT	TAT	TGATT	AGAGAG	AGACAT	GT	1560	
Qy	1561	TATTTTT	CTGGT	AAAAA	CAATCT	TGAT	TAT	GAAC	CTATAT	TAG	TTAGGGAT	1620	
Db	1561	TATTTTT	CTGGT	AAAAA	CAATCT	TGAT	TAT	GAAC	CTATAT	TAG	TTAGGGAT	1620	
Qy	1621	TGTTGT	TCGACAT	AGT	GGTCC	ATT	AAAA	AGAG	GTCT	GAT	TTAAATTTT	1680	
Db	1621	TGTTGT	TCGACAT	AGT	GGTCC	ATT	AAAA	AGAG	GTCT	GAT	TTAAATTTT	1680	
Qy	1681	CACAAAT	CTTTCT	TTT	TAGAAA	TCGG	GACCTG	GGAC	ACCTT	CCT	TACAA	1740	
Db	1681	CACAAAT	CTTTCT	TTT	TAGAAA	TCGG	GACCTG	GGAC	ACCTT	CCT	TACAA	1740	
Qy	1741	ACTAA	CTT	TAC	GTAC	CCCT	CACAT	TCGT	ATACCA	TAAAT	TCAT	1800	
Db	1741	ACTAA	CTT	TAC	GTAC	CCCT	CACAT	TCGT	ATACCA	TAAAT	TCAT	1800	
Qy	1801	TGGT	GAT	CA	TAA	TTT	CGAAA	TA	TTTTT	CA	CTAA	1860	
Db	1801	TGGT	GAT	CA	TAA	TTT	CGAAA	TA	TTTTT	CA	CTAA	1860	
Qy	1861	GGT	ATA	CAT	CA	GAAT	CA	CGAA	AGAA	TTTAA	AAC	1920	
Db	1861	GGT	ATA	CAT	CA	GAAT	CA	CGAA	AGAA	TTTAA	AAC	1920	
Qy	1921	TTTT	GG	CT	TAT	ACT	TTT	TAT	CT	T	GT	1980	
Db	1921	TTTT	GG	CT	TAT	ACT	TTT	TAT	CT	T	GT	1980	
Qy	1981	TATT	CT	TTCT	CT	T	CAAC	AT	CGAA	TTCT	TTT	2040	
Db	1981	TATT	CT	TTCT	CT	T	CAAC	AT	CGAA	TTCT	TTT	2040	

QY	4201	TCGAGGTTCCAGTCAAGCTAGAGTGAAATTCATAGTGGGAACGTGCTCGGATCGCAAAAGT	4260	QY	5281	ATCTTTTAAAGATCTTCAAAGTGTGAGTAGTGTATTTATTTGGTTGGCTTCTGGTGATATTTA	5340
Db	4201	TCGAGGTTCCAGTCAAGCTAGAGTGAAATTCATAGTGGGAACGTGCTCGGATCGCAAAAGT	4260	Db	5281	ATCTTTTAAAGATCTTCAAAGTGTGAGTAGTGTATTTATTTGGTTGGCTTCTGGTGATATTTA	5340
QY	4261	CCCATTTGCCCTGAAGCAGCTCTAAATTTGCCCTAGAGTGTGACTCAACCAATACCTAAAGTTCTG	4320	QY	5341	TGTTTTATTAGAAATTTGGTCTTATATATTTGGCTATATATAGAGGTGTGGGTGATATGAT	5400
Db	4261	CCCATTTGCCCTGAAGCAGCTCTAAATTTGCCCTAGAGTGTGACTCAACCAATACCTAAAGTTCTG	4320	Db	5341	TGTTTTATTAGAAATTTGGTCTTATATATTTGGCTATATATAGAGGTGTGGGTGATATGAT	5400
QY	4321	TTTACTTCAATAAATACTATAGCCTTTACTCAACCTCGCCATTTCTGCCAAAAACATGTCGGTCA	4380	QY	5401	GAAATTCAGAGTGTGAGTGTGGAAACCTTTTGTGTGTTTCATTGAAATTAATCATTCGAATTCCT	5460
Db	4321	TTTACTTCAATAAATACTATAGCCTTTACTCAACCTCGCCATTTCTGCCAAAAACATGTCGGTCA	4380	Db	5401	GAAATTCAGAGTGTGAGTGTGGAAACCTTTTGTGTGTTTCATTGAAATTAATCATTCGAATTCCT	5460
QY	4381	TTGGACAGTGGCGGTTCTTTCAGGAAATGTTTCTGTGTGGAGGAGCTTTAGGAGAACAA	4440	QY	5461	CAATTTCTTGGAGACCCATTTATGAGACATTTGAGACATCTATAGAACATATATGTAATGTA	5520
Db	4381	TTGGACAGTGGCGGTTCTTTCAGGAAATGTTTCTGTGTGGAGGAGCTTTAGGAGAACAA	4440	Db	5461	CAATTTCTTGGAGACCCATTTATGAGACATTTGAGACATCTATAGAACATATATGTAATGTA	5520
QY	4441	GAGAGCAAAATCCAGATCGAAATCTACGGTCTGGTCTCGACTGATATTAATCTACTAGTAC	4500	QY	5521	TATTTAAAACGTACTTAAAGTCGAATTTTATGACCAAAAGTAAAATAAATATATGCCGAATGTACA	5580
Db	4441	GAGAGCAAAATCCAGATCGAAATCTACGGTCTGGTCTCGACTGATATTAATCTACTAGTAC	4500	Db	5521	TATTTAAAACGTACTTAAAGTCGAATTTTATGACCAAAAGTAAAATAAATATATGCCGAATGTACA	5580
QY	4501	TTTCATCACAATCTTCTGCCCCAAGTTTACTCAAAACCTTAGCAAGTTTTCATAGCTACGGTCA	4560	QY	5581	TGCTTAATATCGAGTTTAAACTATTTTTCCTCAATATAACAACCTATTTTCTCTTCGTCCTTTC	5640
Db	4501	TTTCATCACAATCTTCTGCCCCAAGTTTACTCAAAACCTTAGCAAGTTTTCATAGCTACGGTCA	4560	Db	5581	TGCTTAATATCGAGTTTAAACTATTTTTCCTCAATATAACAACCTATTTTCTCTTCGTCCTTTC	5640
QY	4561	AATCCGGAGGTTTAAATTCOAACCTTGGCCATCTTGGCTCTCTCCTCAAAAGCCTTGGAGATT	4620	QY	5641	CTTATATATCTTATTTCTGATTTCTTATTTTCTTCTTTTAAATTCCTTTTCTCTTTTCCCAA	5700
Db	4561	AATCCGGAGGTTTAAATTCOAACCTTGGCCATCTTGGCTCTCTCCTCAAAAGCCTTGGAGATT	4620	Db	5641	CTTATATATCTTATTTCTGATTTCTTATTTTCTTCTTTTAAATTCCTTTTCTCTTTTCCCAA	5700
QY	4621	CAATTCAGCAACACTGGGATTTAGATTTTGTGTGMACTCAAAATAAGCAACATGATAGTGG	4680	QY	5701	GACACAAAAAATAAATAACAGAAAACGAAAAAAGAGATTTTAAAAATTTCAATAACCCAC	5760
Db	4621	CAATTCAGCAACACTGGGATTTAGATTTTGTGTGMACTCAAAATAAGCAACATGATAGTGG	4680	Db	5701	GACACAAAAAATAAATAACAGAAAACGAAAAAAGAGATTTTAAAAATTTCAATAACCCAC	5760
QY	4681	TATGAGTTCTAGTGTGGGATCTTGGATGCATGGAGAAATACCTCCATCAACAAGCTCA	4740	QY	5761	GAGAAATTTATGCTGTCTCAATCATATATGCGCAACTAACTAAATTTGAAAAAGACAATGGAA	5820
Db	4681	TATGAGTTCTAGTGTGGGATCTTGGATGCATGGAGAAATACCTCCATCAACAAGCTCA	4740	Db	5761	GAGAAATTTATGCTGTCTCAATCATATATGCGCAACTAACTAAATTTGAAAAAGACAATGGAA	5820
QY	4741	GCAATTCCTTTCTTGATCAACACTACCGGATTTGGTGAATCTTCAAAACCGGTTATATCC	4800	QY	5821	CGAATTAATATTTGCTTCAATCATATATGCGCAACTAACTAAATTTGAAAAAGACAATGGAA	5880
Db	4741	GCAATTCCTTTCTTGATCAACACTACCGGATTTGGTGAATCTTCAAAACCGGTTATATCC	4800	Db	5821	CGAATTAATATTTGCTTCAATCATATATGCGCAACTAACTAAATTTGAAAAAGACAATGGAA	5880
QY	4801	ATTACTAGAGGTAAAGGAGGTGTTAATCAAGTGATTTCTCAACAGAGAGTAGTGATTA	4860	QY	5881	TGACTGAAACCAATGATATCTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGT	5940
Db	4801	ATTACTAGAGGTAAAGGAGGTGTTAATCAAGTGATTTCTCAACAGAGAGTAGTGATTA	4860	Db	5881	TGACTGAAACCAATGATATCTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGT	5940
QY	4861	TTCCCAATCAGCTAAATGTTTAAAGCCCTTGATGGATTTTCTTCAAGCGGGGTTAGCGCCAC	4920	QY	5941	ACTATCATCATGATTTAGTTAAATGCGATGATCTATATGTTCTTTGAAACATAGATATGTC	6000
Db	4861	TTCCCAATCAGCTAAATGTTTAAAGCCCTTGATGGATTTTCTTCAAGCGGGGTTAGCGCCAC	4920	Db	5941	ACTATCATCATGATTTAGTTAAATGCGATGATCTATATGTTCTTTGAAACATAGATATGTC	6000
QY	4921	GCAACAAGAAATGTGAAGCGGAGAGAAATGATCAGGATCGGGGTAGGGGTAGGGATGG	4980	QY	6001	ATTTATCTGGATATAAAGATGGCGTTTAAACCTACTTTTGCAATTTTGTGTTATATCTTTCT	6060
Db	4921	GCAACAAGAAATGTGAAGCGGAGAGAAATGATCAGGATCGGGGTAGGGGTAGGGATGG	4980	Db	6001	ATTTATCTGGATATAAAGATGGCGTTTAAACCTACTTTTGCAATTTTGTGTTATATCTTTCT	6060
QY	4981	AGTGATTAATCTTCAAGAACTTTTGTGGTAAATCAACATAAATCTCAGGAGGAAACGA	5040	QY	6061	TCTAATACATATGATCAATFACACTTTTGTGTTTAAAGAAAATTAATAAACTTATTTTCAAAC	6120
Db	4981	AGTGATTAATCTTCAAGAACTTTTGTGGTAAATCAACATAAATCTCAGGAGGAAACGA	5040	Db	6061	TCTAATACATATGATCAATFACACTTTTGTGTTTAAAGAAAATTAATAAACTTATTTTCAAAC	6120
QY	5041	GGAATACACATCATGCGGAGGTAAACAGTTCTTGGACCGGTTTCCACCTCCAAACACTCAAC	5100	QY	6121	ATCGATCACATTTTACTTTTCTTCTTCCATATTTGATGATGATGATGATGATGATGATGATGAT	6180
Db	5041	GGAATACACATCATGCGGAGGTAAACAGTTCTTGGACCGGTTTCCACCTCCAAACACTCAAC	5100	Db	6121	ATCGATCACATTTTACTTTTCTTCTTCCATATTTGATGATGATGATGATGATGATGATGATGAT	6180
QY	5101	AGGCCATCTCTCAATCTAAGTACTCAGCACTAGTATTTCTTGATGATTTCTTTTGTGGTT	5160	QY	6181	TTTCGAGATCAGATATCAGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT	6240
Db	5101	AGGCCATCTCTCAATCTAAGTACTCAGCACTAGTATTTCTTGATGATTTCTTTTGTGGTT	5160	Db	6181	TTTCGAGATCAGATATCAGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT	6240
QY	5161	GGGGTGTACATTTGGTCTTGTATGCGAGTTTATGCTGAGGAGATCAAAACCATGCGGT	5220	QY	6241	TTTCCACAGATGTTTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCAT	6300
Db	5161	GGGGTGTACATTTGGTCTTGTATGCGAGTTTATGCTGAGGAGATCAAAACCATGCGGT	5220	Db	6241	TTTCCACAGATGTTTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCAT	6300
QY	5221	ATATCCAAAGGCTAAATTTTGGAGCTCAAGGAAAGGTATGGTTTATAAAACTATCTTTTGG	5280	QY	6301	CTTGAACGATAGCTTTTCTTTTATCGCAATGATGCAATTTGATGAGGCACTCTTCTCTTTT	6360
Db	5221	ATATCCAAAGGCTAAATTTTGGAGCTCAAGGAAAGGTATGGTTTATAAAACTATCTTTTGG	5280	Db	6301	CTTGAACGATAGCTTTTCTTTTATCGCAATGATGCAATTTGATGAGGCACTCTTCTCTTTT	6360

Db 6361 CTACTGTCCTTTTCGATGAAGTACACATAGCTGGCAATGGAATCCGAGAGTTTCCCG 6420
QY 6421 ATATTACCCCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGA 6480
Db 6421 ATATTACCCCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGA 6480
QY 6481 TATTCTTGAGTAGACGAGAGTGTGCTGCTCCACCAATGTTGGGATCTAGATATCACATC 6540
Db 6481 TATTCTTGAGTAGACGAGAGTGTGCTGCTCCACCAATGTTGGGATCTAGATATCACATC 6540
QY 6541 AATCCACTTCTTTGAAAGACGTGTTGGAACGTCTTCTTTTCCACGATGTTCCCTGCG 6600
Db 6541 AATCCACTTCTTTGAAAGACGTGTTGGAACGTCTTCTTTTCCACGATGTTCCCTGCG 6600
QY 6601 GTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCCCT 6660
Db 6601 GTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCCCT 6660
QY 6661 TATCGCAATGATGGCAATTTGTAGAACCAATCTTCTTCTTCTACTGTCTTTCGATGAAGT 6720
Db 6661 TATCGCAATGATGGCAATTTGTAGAACCAATCTTCTTCTTCTACTGTCTTTCGATGAAGT 6720
QY 6721 GACAGATAGCTGGCAATGGAATCCGAGGAGTTTCCCGATATACCTCTTGTGAAAG 6780
Db 6721 GACAGATAGCTGGCAATGGAATCCGAGGAGTTTCCCGATATACCTCTTGTGAAAG 6780
QY 6781 TCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGTATATCTTTGGAGTAGACGAG 6840
Db 6781 TCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGTATATCTTTGGAGTAGACGAG 6840
QY 6841 TGTGCTGCTCCACCATGTTGGGATCTAGATATCAATCAATCCACTTCTTGTGAAGCG 6900
Db 6841 TGTGCTGCTCCACCATGTTGGGATCTAGATATCAATCAATCCACTTCTTGTGAAGCG 6900
QY 6901 TGGTTGGAACGTCTTCTTTTCCACGATGTTCTGCTGGTGGGGTCCATCTTTGGGAC 6960
Db 6901 TGGTTGGAACGTCTTCTTTTCCACGATGTTCTGCTGGTGGGGTCCATCTTTGGGAC 6960
QY 6961 CACTGTCGTAGAGGCATCTTGAACGATAGCCCTTCTTTATCGCAATGATGCAATTTGT 7020
Db 6961 CACTGTCGTAGAGGCATCTTGAACGATAGCCCTTCTTTATCGCAATGATGCAATTTGT 7020
QY 7021 AGAAGCCATCTTCTTTTCTACTGCTTTCGATGAAGTGACAGATAGCTGGGCAATGA 7080
Db 7021 AGAAGCCATCTTCTTTTCTACTGCTTTCGATGAAGTGACAGATAGCTGGGCAATGA 7080
QY 7081 ATCCGAGGAGTTTCCGATATACCTTTGTTGAAAGTCTCAATAGCCCTCTGCTTT 7140
Db 7081 ATCCGAGGAGTTTCCGATATACCTTTGTTGAAAGTCTCAATAGCCCTCTGCTTT 7140
QY 7141 CTGAGACTGTATCTTTGTATATCTTGGAGTAGACGAGAGTGTGCTCCACCATGTTGG 7200
Db 7141 CTGAGACTGTATCTTTGTATATCTTGGAGTAGACGAGAGTGTGCTCCACCATGTTGG 7200
QY 7201 GGATCTAGATATCACATCAATCACTTGTGTTGAGACGTGTTGGAACGTCTTCTTTT 7260
Db 7201 GGATCTAGATATCACATCAATCACTTGTGTTGAGACGTGTTGGAACGTCTTCTTTT 7260
QY 7261 CCACGATGTTCTGCTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTT 7320
Db 7261 CCACGATGTTCTGCTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTT 7320
QY 7321 GAAAGTAGCCCTTCTTCTTATCGCAATGATGGCATTTGTAGAGCCATCTTCTTTTCTA 7380
Db 7321 GAAAGTAGCCCTTCTTCTTATCGCAATGATGGCATTTGTAGAGCCATCTTCTTTTCTA 7380
QY 7381 CTGCTCTTTGATGAAGTACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCGATA 7440
Db 7381 CTGCTCTTTGATGAAGTACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCGATA 7440
QY 7441 TTACCCCTTTGTTGAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATAT 7500

Db 7441 TTACCCCTTTGTTGAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGATAT 7500
QY 7501 TCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTTGGGATCCACTAGTTCTAGAGCG 7560
Db 7501 TCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTTGGGATCCACTAGTTCTAGAGCG 7560
QY 7561 GCCGCCACCGCGGTGGAGCT 7580
Db 7561 GCCGCCACCGCGGTGGAGCT 7580

RESULT 2
ADL71846
ID ADL71846 standard; DNA; 1746 BP.
XX
AC ADL71846;
XX
DT 20-MAY-2004 (first entry)
XX
DE Arabidopsis thaliana OBP3 antisense DNA #7.
XX
KW Transgenic plant; Dof transcription factor; ocs binding factor;
plant size; plant stature; root growth; plant; gene; ds; OBF;
OBF binding protein; OBP3; SOB1; mouse-ear cress.
XX
OS Arabidopsis thaliana.
XX
PN US2004045055-A1.
XX
PD 04-MAR-2004.
XX
PF 28-AUG-2003; 2003US-00650249.
XX
PR 28-AUG-2002; 2002US-0406657P.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Neff MM;
XX
WPI; 2004-225757/21.
XX
New transgenic plant cell, useful in producing plants with altered size
and stature and with normal and healthy root growth.
XX
Claim 38; SEQ ID NO 18; 53pp; English.
XX
The invention relates to a transgenic plant transformed by a Dof
transcription factor, OBF (ocs binding factor) binding protein (OBP3).
OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic
acid and polypeptides are useful in producing transgenic plants with
altered size and stature and with normal and healthy root growth. The
present sequence is Arabidopsis thaliana OBP3 antisense DNA.
XX
SQ Sequence 1746 BP; 560 A; 304 C; 304 G; 578 T; 0 U; 0 Other;

Query Match 19.8%; Score 1503; DB 12; Length 1746;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 4436 AACAGAGAAGCAATCCAGATCGAAATCTACGGTGGTCTCGACTGATAATACTACT 4495
Db 1 AACAGAGAAGCAATCCAGATCGAAATCTACGGTGGTCTCGACTGATAATACTACT 60
QY 4496 AGTACTTCTATCACTTACTTCTCGCCCAAGTTACTCAAAACCCCTAGCAAGTTTCATAGCTAC 4555
Db 61 AGTACTTCTATCACTTACTTCTCGCCCAAGTTACTCAAAACCCCTAGCAAGTTTCATAGCTAC 120
QY 4556 GGTCAAAATCCCGAGGTTAAATTCGAATTTGCCCATCTTGCCTCTCTCCAAAGCCTTGA 4615
Db 121 GGTCAAAATCCCGAGGTTAAATTCGAATTTGCCCATCTTGCCTCTCTCCAAAGCCTTGA 180
QY 4616 GATTACAATTCAAGCAACACTGGATTAGATTTTGGTGGNACTCAATAGCAACATGATA 4675

Db	181	GATTACAATTC	AAGCAAC	ACTGGA	TTAGATTTTGGTGGAACTC	CAATAAGCAAC	ATGATA	240
Qy	4676	AGTGGTATGAG	TCTTAGTGGTGGGATCTTTGGATG	CAATGAGAA	TACCTCCATCA	CAACAA	4735	
Db	241	AGTGGTATGAG	TCTTAGTGGTGGATCTTTGGATG	CAATGAGAA	TACCTCCATCA	CAACAA	300	
Qy	4736	GCTCAGCAAT	TCCGTTTCTTGATCAAC	CACTACCGGATTTGGTGC	AAATCTTCAAACGGGT	TTA	4795	
Db	301	GCTCAGCAAT	TCCGTTTCTTGATCAAC	CACTACCGGATTTGGTGC	AAATCTTCAAACGGGT	TTA	360	
Qy	4796	TATCCATTA	CTAGAGTAAAGGAGGCTGTTAA	TCAAGGTGATTTCTCAACAGAA	GAGTACTG	4855		
Db	361	TATCCATTA	CTAGAGGTAAGGAGGCTGTTAA	TCAAGGTGATTTCTCAACAGAA	GAGTACTG	420		
Qy	4856	GATTATTTCCAA	TCAAGCTAAATGTTTAAAGCCCTTCATG	ATATTTCTTTCAGCGGGGT	TAGC	4915		
Db	421	GATTATTTCCAA	TCAAGCTAAATGTTTAAAGCCCTTCATG	ATATTTCTTTCAGCGGGGT	TAGC	480		
Qy	4916	GCCACGCAAA	CAGAAATGTAAAGCGGGAAGAGAA	TGATCAGATCGGGGTAGG	ATGCGG	4975		
Db	481	GCCACGCAAA	CAGAAATGTAAAGCGGGAAGAGAA	TGATCAGATCGGGGTAGG	ATGCGG	540		
Qy	4976	GATGGAGTGA	ATAACTTATCAAGAACTTTTTCGGTAA	TATCAACAATAACTCAG	CGCAGG	5035		
Db	541	GATGGAGTGA	ATAACTTATCAAGAACTTTTTCGGTAA	TATCAACAATAACTCAG	CGCAGG	600		
Qy	5036	AACGAGGAAT	ACATCATCGGGAGGTAA	CAGTCTTGGACCGGTTTCACTCCAA	CAAC	5095		
Db	601	AACGAGGAAT	ACATCATCGGGAGGTAA	CAGTCTTGGACCGGTTTCACTCCAA	CAAC	660		
Qy	5096	TCAACAGGCC	ATCTCTCATTC	---TAAGTACTCAGCACTAGCTAT	TCTTGATGATTTCTTT	5152		
Db	661	TCAACAGGCC	ATCTCTCATTC	---TAAGTACTCAGCACTAGCTAT	TCTTGATGATTTCTTT	720		
Qy	5153	TGTTGGTTGGG	GTGTACATTTGGTCTTGT	CAATCGGAGTTATTCCTGAGNAGATCA	CAACC	5212		
Db	721	TGTTGGTTGGG	GTGTACATTTGGTCTTGT	CAATCGGAGTTATTCCTGAGNAGATCA	CAACC	780		
Qy	5213	ATGCAGCTAT	ATCCAAAGGCTAA	TTTTTGAGGCTCAAAAGGAAGTATGGTTA	TAAAACTA	5272		
Db	781	ATGCAGCTAT	ATCCAAAGGCTAA	TTTTTGAGGCTCAAAAGGAAGTATGGTTA	TAAAACTA	840		
Qy	5273	TCCTTTTGTAT	CTTTTAAAGATCTTCAAAGTGTGAGTATG	TTTATTTGGTTGGCTTCTGGT	5332			
Db	841	TCCTTTTGTAT	CTTTTAAAGATCTTCAAAGTGTGAGTATG	TTTATTTGGTTGGCTTCTGGT	900			
Qy	5333	GATATTTATG	TTTTTATAGAA	TTTGGTCTTATATATTTGGCTATATATAGAGGTGTGGGTG	5392			
Db	901	GATATTTATG	TTTTTATAGAA	TTTGGTCTTATATATTTGGCTATATATAGAGGTGTGGGTG	960			
Qy	5393	ATATGTATGA	NTTCAAGAGTTGATGTGGAA	CACTTTTGTGTGTTTCATTTGAATATATCAT	5452			
Db	961	ATATGTATGA	NTTCAAGAGTTGATGTGGAA	CACTTTTGTGTGTTTCATTTGAATATATCAT	1020			
Qy	5453	CGAATTTCTCA	ATTTCTTGGAGACCACTTATGAGACATTTGAGACATCTATAGAACATATAT	5512				
Db	1021	CGAATTTCTCA	ATTTCTTGGAGACCACTTATGAGACATTTGAGACATCTATAGAACATATAT	1080				
Qy	5513	GTAATGTAT	ATAA	CGPTTAAGT	CGAAATTTTATGACCAAGTAATATAATATGCGG	5572		
Db	1081	GTAATGTAT	ATAA	CGPTTAAGT	CGAAATTTTATGACCAAGTAATATAATATGCGG	1140		
Qy	5573	AATGTACATG	CTAATATCGAGTTTAAACTATTTTTTCCATATAA	CAACTATTTTCTCTTTT	5632			
Db	1141	AATGTACATG	CTAATATCGAGTTTAAACTATTTTTTCCATATAA	CAACTATTTTCTCTTTT	1200			
Qy	5633	TGCTCCAA	CTTATATAC	TCTTATCTGATTTCTTCTTTTAAATTCCTTTTCC	5692			
Db	1201	TGCTCCAA	CTTATATAC	TCTTATCTGATTTCTTCTTTTAAATTCCTTTTCC	1260			
Qy	5693	TTTCCCAAG	ACACAAAAA	AAAAAATA	CAGAAA	CGAAAAAAGAGATTTTAAAAATCA	5752	
Db	1261	TTTCCCAAG	ACACAAAAA	AAAAAATA	CAGAAA	CGAAAAAAGAGATTTTAAAAATCA	1320	

QY	5753	TAACCCACGAGAAATTATGCACCTAAATTCAGACTTAATCCCCCAAAATTCAGAAAATTTATG	5813
DB	1321	TAACCCACGAGAAATTATGCACCTAAATTCAGACTTAATCCCCCAAAATTCAGAAAATTTATG	1380
QY	5813	TATTTTTCGCAATTAATATTTGTGTTCAATCATATAATATGGCCAACTAACTAAATTTGAAAAGA	5872
DB	1381	TATTTTTCGCAATTAATATTTGTGTTCAATCATATAATGGCCAACTAACTAAATTTGAAAAGA	1440
QY	5873	CAATGGAAATGACTGAAACCAATGCATATAATCTCTCAAGCTCTCAACCTATGAAGAATCATGTA	5932
DB	1441	CAATGGAAATGACTGAAACCAATGCATATAATCTCTCAAGCTCTCAACCTATGAAGAATCATGTA	1500
QY	5933	ACCAATAGACTATCATCATGATTAGTTTAATGCGATGATCTATAATGTATTTCTTTGAAACATA	5992
DB	1501	ACCAATAGACTATCATCATGATTAGTTTAATGCGATGATCTATAATGTATTTCTTTGAAACATA	1560
QY	5993	GATATGCACTTTATCTGGATATATAAGATGGCGTTTAAACCTACTTTTGCAATTTTGTGTAT	6052
DB	1561	GATATGCTAATTTATCTGGATATATAAGATGGCGTTTAAACCTACTTTTGCAATTTTGTGTAT	1620
QY	6053	ATCTTTCTCTTAATACATATATGATCAATACACTTTTGTGTTTTTAAAGAAATTAATAAACTTA	6112
DB	1621	ATCTTTCTCTTAATACATATATGATCAATACACTTTTGTGTTTTTAAAGAAATTAATAAACTTA	1680
QY	6113	TTTCAAACATCGATCACAATTTTACTTTTGTGTTTCCATATTTGACTACATTTATATAGGCTCAC	6172
DB	1681	TTTCAAACATCGATCACAATTTTACTTTTGTGTTTCCATATTTGACTACATTTATATAGGCTCAC	1740
QY	6173	ACTTTT 6178	
DB	1741	ACTTTT 1746	

RESULT 3
ABQ73047/c
ID ABQ73047 standard; DNA; 10078 BP.
XX AC
XX AC ABQ73047;
XX DT
XX 24-SEP-2002 (first entry)
XX DE Tomato anthocyanin 1 (ANT1) related plasmid pAG3202 SEQ ID NO:3.
XX KW
XX Tomato; ANT1; anthocyanin 1; Lycopersicon esculentum; plant; colour;
XX gene; ds.
XX OS
XX Lycopersicon esculentum.
XX OS Synthetic.
XX PN
XX WO200255658-A2.
XX PD
XX 18-JUL-2002.
XX PF
XX 29-OCT-2001; 2001WO-US050638.
XX PR
XX 30-OCT-2000; 2000US-0244685P.
XX PA (EXEL-) EXELIXIS PLANT SCI INC.
XX PI
XX Connors K, Mathews HV, Liu A;
XX WPI; 2002-557819/59.
XX DR
XX New isolated polynucleotide derived from tomato, useful for producing an
XX PT Anthocyanin 1 phenotype in plants, particularly for modifying e.g. leaf
XX PT color, flower color or fruit color in plants.
XX PS
XX Example 1; Page 41-46; 53pp; English.
XX CC
XX The present invention describes tomato anthocyanin 1 (ANT1). The ANT1
XX CC polynucleotide can be used for modifying the expression of a native plant
XX CC gene, particularly for producing an anthocyanin 1 phenotype in plants,

CC which is responsible for many red and blue colours in plants. The
CC polynucleotide is useful for modifying e.g. leaf colour, flower colour or
CC fruit colour in plants. The present sequence represents the plasmid
CC pAG3202 which is used in an example from the present invention for the
CC generation of plants with an AN1 phenotype by transformation with an
CC activation tagging construct
XX
SQ Sequence 10078 BP; 2533 A; 2568 C; 2625 G; 2333 T; 0 U; 19 Other;

Query Match 18.5%; Score 1402; DB 6; Length 10078;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	6179	GTTCGGATCTAGATATCACAATCCACTTCTTTGAAGACGTGGTTGGAACGTCCTTC	6238
DB	4249	GTTCGGATCTAGATATCACAATCCACTTCTTTGAAGACGTGGTTGGAACGTCCTTC	4190
QY	6239	TTTTTCCACGATGTTCCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGC	6298
DB	4189	TTTTTCCACGATGTTCCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGC	4130
QY	6299	ATCTTGAAGATAGCCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTCTT	6358
DB	4129	ATCTTGAAGATAGCCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTCTT	4070
QY	6359	TTCTACTGTCCTTTCGAAGATGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCC	6418
DB	4069	TTCTACTGTCCTTTCGAAGATGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCC	4010
QY	6419	CGATATTACCCCTTTGTTGAAGATCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT	6478
DB	4009	CGATATTACCCCTTTGTTGAAGATCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT	3950
QY	6479	GATATTCTTGGAGTAGACAGAGTGTCTGCTCCACCATGTTGGGATCTAGATATCACA	6538
DB	3949	GATATTCTTGGAGTAGACAGAGTGTCTGCTCCACCATGTTGGGATCTAGATATCACA	3890
QY	6539	TCAATCCACTTGTGGAAGACGTGGTTGGAACGTCCTTTTTCACGATGTTCTCGT	6598
DB	3889	TCAATCCACTTGTGGAAGACGTGGTTGGAACGTCCTTTTTCACGATGTTCTCGT	3830
QY	6599	GGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCCTTCC	6658
DB	3829	GGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCCTTCC	3770
QY	6659	TTTATCGCAATGATGCCATTTGTAGAAGCATCTTCTTTTCTACTGTCCTTTTCCGATGA	6718
DB	3769	TTTATCGCAATGATGCCATTTGTAGAAGCATCTTCTTTTCTACTGTCCTTTTCCGATGA	3710
QY	6719	GTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCGATATTAACCTTTGTTGAAA	6778
DB	3709	GTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCGATATTAACCTTTGTTGAAA	3650
QY	6779	AGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTTGATATTTCTGGAGTAGACG	6838
DB	3649	AGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTTGATATTTCTGGAGTAGACG	3590
QY	6839	AGTGTGCTGCTCCACCATGTTGGGATCTAGATATCACAATCCACTTGTCTTTGAAGA	6898
DB	3589	AGTGTGCTGCTCCACCATGTTGGGATCTAGATATCACAATCCACTTGTCTTTGAAGA	3530
QY	6899	CGTGGTTGGAAGCTCTTCTTTTCCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTGGG	6958
DB	3529	CGTGGTTGGAAGCTCTTCTTTTCCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTGGG	3470
QY	6959	ACCACTGTCGGTAGAGGCATCTTGAACGATAGCTTTCCTTTATCGCAATGATGGCATTT	7018
DB	3469	ACCACTGTCGGTAGAGGCATCTTGAACGATAGCTTTCCTTTATCGCAATGATGGCATTT	3410
QY	7019	GTAGAAGCCATCTTCTCTTCTACTGTCCTTTTCGATGAAGTGCACAGATAGCTGGCAATG	7078
DB	3409	GTAGAAGCCATCTTCTCTTCTACTGTCCTTTTCGATGAAGTGCACAGATAGCTGGCAATG	3350

QY	7079	GAATCCGAGGAGGTTTCCGATATTACCCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTC	7138
DB	3349	GAATCCGAGGAGGTTTCCGATATTACCCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTC	3290
QY	7139	TTCTCAGACTGTATCTTTTGATATTTCTTGAGTAGACGAGAGTGTCTGCTCCACCATGTT	7198
DB	3289	TTCTCAGACTGTATCTTTTGATATTTCTTGAGTAGACGAGAGTGTCTGCTCCACCATGTT	3230
QY	7199	GGGGATCTAGATATCACAATCCACTTGTCTTTGAAGACGTGGTTGGAACGTCCTCTTT	7258
DB	3229	GGGGATCTAGATATCACAATCCACTTGTCTTTGAAGACGTGGTTGGAACGTCCTCTTT	3170
QY	7259	TTCTCAGACTGTCTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATC	7318
DB	3169	TTCTCAGACTGTCTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATC	3110
QY	7319	TTGAACGATAGCTTCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTTC	7378
DB	3109	TTGAACGATAGCTTCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTTC	3050
QY	7379	TACTGTCTTTCGATGAAGTGAAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGA	7438
DB	3049	TACTGTCTTTCGATGAAGTGAAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGA	2990
QY	7439	TATTACCCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT	7498
DB	2989	TATTACCCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT	2930
QY	7499	ATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCCACTAGTCTTAGAG	7558
DB	2929	ATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCCACTAGTCTTAGAG	2870
QY	7559	CGGCCGCCACCGCGTGGAGCT 7580	
DB	2869	CGGCCGCCACCGCGTGGAGCT 2848	

RESULT 4
ADV39061/c
ID ADV39061 standard; DNA; 17511 BP.
XX
AC ADV39061;
XX
XX 24-FEB-2005 (first entry)
XX
DE Plant gene activation vector-related DNA sequence pHR-AT - SEQ ID 13.
XX
KW gene activation vector; genetic analysis; ds.
XX
OS Unidentified.
XX
XX WO2004106520-A1.
XX
PD 09-DEC-2004.
XX
XX 28-MAY-2004; 2004WO-JP007789.
XX
XX 30-MAY-2003; 2003JP-00153985.
XX
XX (RIKE) RIKEN KK.
XX
XX Muranaka T, Seki H;
XX
XX WPI; 2005-021291/02.
XX
PT Novel plant gene active vector comprising hairy-root induction gene, and
PT enhancer and/or promoter that functions in plant, useful for activating
PT plant gene forming hairy root.
XX
PS Claim 4; SEQ ID NO 13; 54pp; Japanese.
XX
XX The invention comprises a plant gene activation vector that contains a
CC hairy-root induction gene and enhancer and/or promoter which can function

CC in a plant. The vector of the invention is useful for analyzing a plant
CC gene. The present DNA sequence is claimed in the invention.
XX
SQ Sequence 17511 BP; 4453 A; 4201 C; 4511 G; 4344 T; 0 U; 2 Other;
Query Match 18.0%; Score 1367; DB 14; Length 17511;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6179 GTTTCGGATCTAGATATACATCAATCCACTTCTTTGAAGACGTTGGAAACGTCCTTC 6238
DB 17503 GTTTCGGATCTAGATATACATCAATCCACTTCTTTGAAGACGTTGGAAACGTCCTTC 17444
QY TTTTTCACAGATGTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGGTAGAGGC 6298
DB 17443 TTTTTCACAGATGTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGGTAGAGGC 17384
QY 6299 ATCTTGAAGCATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCCTT 6358
DB 17383 ATCTTGAAGCATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCCTT 17324
QY 6359 TTCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCC 6418
DB 17323 TTCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCC 17264
QY 6419 CGATATTACCTTTGTTGAAAAGTCTCAATAGCCCTCGGTCTTCTGAGACTGTATCTTT 6478
DB 17263 CGATATTACCTTTGTTGAAAAGTCTCAATAGCCCTCGGTCTTCTGAGACTGTATCTTT 17204
QY 6479 GATATCTTGGAGTAGACAGAGTGTGCTGCTCCACCATGTTGGGATCTAGATATCACA 6538
DB 17203 GATATCTTGGAGTAGACAGAGTGTGCTGCTCCACCATGTTGGGATCTAGATATCACA 17144
QY 6539 TCAATCCACTTGTGGAAGACGTGTTGGAAAGTCTTCTTTTCCACGATGTTCTCGT 6598
DB 17143 TCAATCCACTTGTGGAAGACGTGTTGGAAAGTCTTCTTTTCCACGATGTTCTCGT 17084
QY 6599 GGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCACTGTGAACGATGACCTTTCC 6658
DB 17083 GGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCACTGTGAACGATGACCTTTCC 17024
QY 6659 TTTATCGCAATGATGCACTTTGTAGAAGCCATCTTCTTTTCTACTGTCCTTTCCGATGAA 6718
DB 17023 TTTATCGCAATGATGCACTTTGTAGAAGCCATCTTCTTTTCTACTGTCCTTTCCGATGAA 16964
QY 6719 GTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCTTTGTTGAAA 6778
DB 16963 GTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCTTTGTTGAAA 16904
QY 6779 AGTCTCAATAGCCCTCTGGTCTTTCTGAGACTGTATCTTTGATATTTCTGGAGTAGACGAG 6838
DB 16903 AGTCTCAATAGCCCTCTGGTCTTTCTGAGACTGTATCTTTGATATTTCTGGAGTAGACGAG 16844
QY 6839 AGTCTGCTCTCCACCATGTTGGGATCTAGATATCACATCAATCCACTTGTCTTGAAGA 6898
DB 16843 AGTCTGCTCTCCACCATGTTGGGATCTAGATATCACATCAATCCACTTGTCTTGAAGA 16784
QY 6899 CGTGGTTGGAACGTCCTTTTCCACGATGTTTCTCGTGGGTGGGGTCCATCTTTTGGG 6958
DB 16783 CGTGGTTGGAACGTCCTTTTCCACGATGTTTCTCGTGGGTGGGGTCCATCTTTTGGG 16724
QY 6959 ACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCTTTATCCCAATGATGGCATTT 7018
DB 16723 ACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCTTTATCCCAATGATGGCATTT 16664
QY 7019 GTAGAGCCATCTTCTTTTCTACTCTCTTTCGATGAAGTGACAGATAGCTGGGCAATG 7078
DB 16663 GTAGAGCCATCTTCTTTTCTACTCTCTTTCGATGAAGTGACAGATAGCTGGGCAATG 16604
QY 7079 GAATCCGAGGAGTTTCCCGATATTACCTTTTGTGAAAAGTCTCAATAGCCCTCTGGTC 7138
DB 16603 GAATCCGAGGAGTTTCCCGATATTACCTTTTGTGAAAAGTCTCAATAGCCCTCTGGTC 16544

QY 7139 TTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTT 7198
DB 16543 TTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTT 16484
QY 7199 GGGGATCTAGATATCACATCAATCCACTTGTCTTTGAAGACGTTGGAAACGTCCTTTCTTT 7258
DB 16483 GGGGATCTAGATATCACATCAATCCACTTGTCTTTGAAGACGTTGGAAACGTCCTTTCTTT 16424
QY 7259 TTCCACGATGTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGGTAGAGGCATC 7318
DB 16423 TTCCACGATGTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGCGGTAGAGGCATC 16364
QY 7319 TTGAACGATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTTC 7378
DB 16363 TTGAACGATAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTTC 16304
QY 7379 TACTGTCCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGA 7438
DB 16303 TACTGTCCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGA 16244
QY 7439 TATTACCCCTTTGTGAAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGAT 7498
DB 16243 TATTACCCCTTTGTGAAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGAT 16184
QY 7499 ATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCC 7545
DB 16183 ATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGATCC 16137

RESULT 5
ADV39062/c
ID ADV39062 standard; DNA; 18987 BP.
XX
AC ADV39062;
XX
DT 24-FEB-2005 (first entry)
XX
DE Plant gene activation vector-related DNA sequence pHR-AT-GFP - SEQ ID 14.
XX
KW gene activation vector; genetic analysis; ds.
XX
OS Unidentified.
XX
PN WO2004106520-A1.
XX
PD 09-DEC-2004.
XX
PF 28-MAY-2004; 2004WO-JP007789.
XX
PR 30-MAY-2003; 2003JP-00153985.
XX
PA (RIKE) RIKEN KK.
XX
PI Muranaka T, Seki H;
XX
DR WPI; 2005-021291/02.
XX
PT Novel plant gene active vector comprising hairy-root induction gene, and
PT enhancer and/or promoter that functions in plant, useful for activating
PT plant gene forming hairy root.
PS Claim 5; SEQ ID NO 14; 54pp; Japanese.
XX
CC The invention comprises a plant gene activation vector that contains a
CC hairy-root induction gene and enhancer and/or promoter which can function
CC in a plant. The vector of the invention is useful for analyzing a plant
CC gene. The present DNA sequence is claimed in the invention.
XX
SQ Sequence 18987 BP; 4871 A; 4609 C; 4863 G; 4642 T; 0 U; 2 Other;

Query Match 18.0%; Score 1367; DB 14; Length 18987;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	6179	GTTCGGATCTAGATATCAATCAATCCACTTCTTGTGAAGACGTGGTGGAACTGCTTC	6238
Db	18979	GTTCGGATCTAGATATCAATCAATCCACTTCTTGTGAAGACGTGGTGGAACTGCTTC	18920
QY	6239	TTTTCCTCAGATGTTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGCTGGTAGAGC	6298
Db	18919	TTTTCCTCAGATGTTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGCTGGTAGAGC	18860
QY	6299	ATCTTGAAGATAGCTTCTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCCTT	6358
Db	18859	ATCTTGAAGATAGCTTCTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCCTT	18800
QY	6359	TTCTACTGCTCTTTCGATGAAGTGAAGATGAGTGGGCAATGGAATCCGAGAGGTTTCC	6418
Db	18799	TTCTACTGCTCTTTCGATGAAGTGAAGATGAGTGGGCAATGGAATCCGAGAGGTTTCC	18740
QY	6419	CGATATTACCTTTGTTGAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT	6478
Db	18739	CGATATTACCTTTGTTGAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT	18680
QY	6479	GATATTCTTGGAGTAGACAGAGTGTCTGCTCCACCCTGTTGGGATCTAGATATCACA	6538
Db	18679	GATATTCTTGGAGTAGACAGAGTGTCTGCTCCACCCTGTTGGGATCTAGATATCACA	18620
QY	6539	TCAATCCAATGCTTTGGAAGACGTGGTTGGAAAGTCTTCTTTTCCACGATGTTCTGCT	6598
Db	18619	TCAATCCAATGCTTTGGAAGACGTGGTTGGAAAGTCTTCTTTTCCACGATGTTCTGCT	18560
QY	6599	GGGTGGGGTCCATCTTTGGGACCACTGCTGGTAGAGGATCTTGAACGATAGCTTTCC	6658
Db	18559	GGGTGGGGTCCATCTTTGGGACCACTGCTGGTAGAGGATCTTGAACGATAGCTTTCC	18500
QY	6659	TTTATCGCAATGATGCAATTTGTGAAGCCATCTTCTTTTCTACTGCTCTTTCGATGAA	6718
Db	18499	TTTATCGCAATGATGCAATTTGTGAAGCCATCTTCTTTTCTACTGCTCTTTCGATGAA	18440
QY	6719	GTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCGATATPACCTTTGTTGAAA	6778
Db	18439	GTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCGATATPACCTTTGTTGAAA	18380
QY	6779	AGTCTCAATAGCCCTGCTCTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAG	6838
Db	18379	AGTCTCAATAGCCCTGCTCTCTGAGACTGTATCTTTGATATCTTGGAGTAGACGAG	18320
QY	6839	AGTGTGCTGCTCCACCATGTTGGGATCTAGATATCACATCAATCCACTTGTCTTGAAGA	6898
Db	18319	AGTGTGCTGCTCCACCATGTTGGGATCTAGATATCACATCAATCCACTTGTCTTGAAGA	18260
QY	6899	CGTGTGTGAACGTCTTCTTTTCCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTGGG	6958
Db	18259	CGTGTGTGAACGTCTTCTTTTCCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTGGG	18200
QY	6959	ACCAGTGTGGTAGAGGATCTTGAACGATAGCTTCTTATCGCAATGATGGCAATTT	7018
Db	18199	ACCAGTGTGGTAGAGGATCTTGAACGATAGCTTCTTATCGCAATGATGGCAATTT	18140
QY	7019	GTAGAAGCCATCTTCTCTTCTACTGCTCTTTCGATGAAGTGCACAGATAGCTGGGCAATG	7078
Db	18139	GTAGAAGCCATCTTCTCTTCTACTGCTCTTTCGATGAAGTGCACAGATAGCTGGGCAATG	18080
QY	7079	GAATCCGAGAGGTTTCCGATATPACCTTTTGTGAAGTCTCAATAGCCCTCTGCTTC	7138
Db	18079	GAATCCGAGAGGTTTCCGATATPACCTTTTGTGAAGTCTCAATAGCCCTCTGCTTC	18020
QY	7139	TTCTGAGACTGTATCTTTGATATCTTGTGAGTAGACGAGTGTGCTGCCACCATGTT	7198
Db	18019	TTCTGAGACTGTATCTTTGATATCTTGTGAGTAGACGAGTGTGCTGCCACCATGTT	17960
QY	7199	GGGGATCTAGATATCACATCAATCCACTTGTCTTGAAGACGTGGTGGAACTGCTCTTT	7258
Db	17959	GGGGATCTAGATATCACATCAATCCACTTGTCTTGAAGACGTGGTGGAACTGCTCTTT	17900

QY	7259	TTCCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTGGGACCACTGCTGGTAGAGGATC	7318
Db	17899	TTCCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTGGGACCACTGCTGGTAGAGGATC	17840
QY	7319	TTGAAAGATAGCTTCTTTCCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTC	7378
Db	17839	TTGAAAGATAGCTTCTTTCCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTC	17780
QY	7379	TACTGTCTTTCGATGAAGTGCACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGA	7438
Db	17779	TACTGTCTTTCGATGAAGTGCACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGA	17720
QY	7439	TATTACCCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT	7498
Db	17719	TATTACCCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT	17660
QY	7499	ATTCTTGGAGTAGACAGAGTGTCTGCTCCACCCTGTTGGGATCC	7545
Db	17659	ATTCTTGGAGTAGACAGAGTGTCTGCTCCACCCTGTTGGGATCC	17613

RESULT 6
AAA88401/c
ID AAA88401 standard; DNA; 1361 BP.
XX
AC AAA88401;
XX
DT 09-JAN-2001 (first entry)
XX
DE 4X CaMV 35S enhancer construct.
XX
KW CaMV; 35S; enhancer; trait-associated gene identification;
KW activation tagging; fruit; transgenic plant; ss.
OS Cauliflower mosaic virus.
XX
FH Key Location/Qualifiers
FT repeat_region 1..1354
FT /tag= a
FT /repeat_type= TANDEM
FT /note= "4 CaMV 35S enhancer units"
FT repeat_unit 1..339
FT /tag= b
FT /note= "CaMV 35S enhancer unit 1"
FT enhancer 1..129
FT /tag= c
FT /note= "CaMV 35S enhancer AluI-EcoRV fragment"
FT enhancer 130..331
FT /tag= d
FT /note= "129 bp fragment of the CaMV sequence"
FT enhancer 333..339
FT /tag= e
FT /note= "additional 7 bp not associated with 35S enhancer"
FT repeat_unit 340..678
FT /tag= f
FT /note= "CaMV 35S enhancer unit 2"
FT enhancer 340..541
FT /tag= g
FT /note= "CaMV 35S enhancer AluI-EcoRV fragment"
FT enhancer 542..670
FT /tag= h
FT /note= "129 bp fragment of the CaMV sequence"
FT enhancer 672..678
FT /tag= i
FT /note= "additional 7 bp not associated with 35S enhancer"
FT repeat_unit 679..1017
FT /tag= j
FT /note= "CaMV 35S enhancer unit 3"
FT enhancer 679..880
FT /tag= k
FT /note= "CaMV 35S enhancer AluI-EcoRV fragment"
FT enhancer 881..1009
FT /tag= l

FT	enhancer	/note= "129 bp fragment of the CaMV sequence"	
FT		1011. .1017	
FT		/*tag= m	
FT	repeat_unit	/note= "Additional 7 bp not associated with 35S enhancer"	
FT		1018. .1354	
FT		/*tag= a	
FT	enhancer	/note= "CaMV 35S enhancer unit 4"	
FT		1018. .1219	
FT		/*tag= n	
FT	enhancer	/note= "CaMV 35S enhancer AluI-EcoRV fragment"	
FT		1220. .1348	
FT		/*tag= o	
FT	enhancer	/note= "129 bp fragment of the CaMV sequence"	
FT		1350. .1354	
FT		/*tag= p	
FT		/note= "Additional 6 bp not associated with 35S enhancer"	
XX	WO200053794-A2.		
XX	14-SEP-2000.		
XX	09-MAR-2000; 2000WO-US006298.		
XX	12-MAR-1999; 99US-0124232P.		
XX	(AGRI-) AGRITOPE INC.		
XX	Wagner R, Mathews H, Liu XL, Waggoner WJ;		
XX	WPI; 2000-594336/56.		
XX	Identifying genes associated with a desired trait for isolating and		
PT	characterizing the genes comprises using an enhancer element which		
PT	enhances gene expression and stably integrates into the plant genome.		
XX	Claim 4; Fig 5; 42pp; English.		
XX	The present sequence is that of a 4X cauliflower mosaic virus (CaMV) 35S		
CC	enhancer sequence preferred for use in the method of the invention. It		
CC	includes 4 repeats of 202 bp AluI-EcoRV fragments of the 35S enhancer,		
CC	129 bp of the CaMV sequence associated with each tandem Alu-EcoRV repeat,		
CC	and an additional 7 bp repeated sequence, which does not appear in the		
CC	35S enhancer region of the native CaMV genome. This 4X CaMV 35S enhancer		
CC	element can be used in a method for identifying genes associated with a		
CC	desired trait in a fruit-bearing plant. The method involves: transforming		
CC	plant cells with an activation tagging vector comprising an element which		
CC	functions to enhance gene expression and has the ability to integrate		
CC	into the plant genome in a manner effective to enhance expression of		
CC	native plant genes, selecting transformed plant cells, regenerating		
CC	transformed plant cells to yield mature plants, selecting plants having a		
CC	desired trait, identifying, isolating and characterizing genes the		
CC	transcription of which has been enhanced, and confirming the contribution		
CC	of the modified expression of each identified gene to the desired trait.		
CC	The desired trait may be increased resistance to fungal, bacterial or		
CC	viral pathogens, insects, modifications in flower size, flower number,		
CC	flower pigmentation and shape, modified leaf number, leaf pigmentation		
CC	and shape, modified seed number, pattern or distribution of leaves and		
CC	flowers, modified stem length between nodes, root mass or root		
CC	development characteristics or increased drought, salt and antibiotic		
CC	tolerance. Plants having short life cycles are transformed, as		
CC	exemplified by dwarf varieties of tomato		
XX			
SQ	Sequence 1361 BP; 447 A; 332 C; 297 G; 285 T; 0 U; 0 Other;		
	Query Match 17.9%; Score 1360; DB 3; Length 1361;		
	Best Local Similarity 100.0%; Pred. No. 0;		
	Matches 1360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	6179 GTTTCGGATCTAGATATCACATCAATCCACTTCTTTGAAGACGTGGTGGAAACGTCCTC		6238
Db	1360 GTTTCGGATCTAGATATCACATCAATCCACTTCTTTGAAGACGTGGTGGAAACGTCCTC		1301
QY	6239 TTTTTCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTGGGACCACCTGTCGGTAGGCG		6298

1300	TTTTTCCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTGGACCACTGTCGCTGAGGC	1241
6299	ATCTTGAAGATAGCTTTCTTTATCCAAATGAGGCAATTTGTAGAGCCATCTTCTCTT	6358
1240	ATCTTGAAGATAGCTTTCTTTATCGAAATGATGGCAATTTGTAGAGCCATCTTCTCTT	1181
6359	TTCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTC	6418
1180	TTCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTC	1121
6419	CGATATTACCTTTGTTGAAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT	6478
1120	CGATATTACCTTTGTTGAAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT	1061
6479	GATATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCACA	6538
1060	GATATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCACA	1001
6539	TCAATCCACTTGTCTTTGAAGACGTGTTGGAACGTCTTCTTTTCCACGATGTTCTCGT	6598
1000	TCAATCCACTTGTCTTTGAAGACGTGTTGGAACGTCTTCTTTTCCACGATGTTCTCGT	941
6599	GGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCCTTC	6658
940	GGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCCTTC	881
6659	TTTATCGCAATGATGGCAATTTGTAGAGGCATCTTCTTTTCTACTGCTTTTCGATGAA	6718
880	TTTATCGCAATGATGGCAATTTGTAGAGGCATCTTCTTTTCTACTGCTTTTCGATGAA	821
6719	GTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTCCTCCGATATTTACCCTTTGTGAAA	6778
820	GTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTCCTCCGATATTTACCCTTTGTGAAA	761
6779	AGTCTCAATAGCCCTCTGCTTTTCCACGATGTTCTCTGAGACTGTATCTTTGATATTTCT	6838
760	AGTCTCAATAGCCCTCTGCTTTTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAG	701
6839	AGTGTGCTGCTCACCATGTTGGGATCTAGATATCACATCAATCCACTTGTGTTGAA	6898
700	AGTGTGCTGCTCACCATGTTGGGATCTAGATATCACATCAATCCACTTGTGTTGAA	641
6899	CCTGTTGGAACGTCTTCTTTTCCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTGGG	6958
640	CCTGTTGGAACGTCTTCTTTTCCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTGGG	581
6959	ACCACCTGTCGGTAGAGGCATCTTGAACGATAGCCCTTTCTTTATCGCAATGATGGCATTT	7018
580	ACCACCTGTCGGTAGAGGCATCTTGAACGATAGCCCTTTCTTTATCGCAATGATGGCATTT	521
7019	GTAGAAGCCATCTTCTTTTCTGTCCTTTTCGATGAAGTAGACAGATAGCTGGGCAATG	7078
520	GTAGAAGCCATCTTCTTTTCTGTCCTTTTCGATGAAGTAGACAGATAGCTGGGCAATG	461
7079	GATCCGAGAGGTTCCTCGATATTTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTC	7138
460	GATCCGAGAGGTTCCTCGATATTTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTC	401
7139	TTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAGAGTGTCTGTCCTCAATGTT	7198
400	TTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAGAGTGTCTGTCCTCAATGTT	341
7199	GGGATCTAGATATCACATCAATCCACTTGTCTTTGAAGACGTGGTGGAAACGTCCTTTT	7258
340	GGGATCTAGATATCACATCAATCCACTTGTCTTTGAAGACGTGGTGGAAACGTCCTTTT	281
7259	TTCCACGATGTTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCATC	7318
280	TTCCACGATGTTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCATC	221
7319	TTGAACGATAGCCCTTTCTTTTATCGCAATGATGGCAATTTGTAGAACCACTTCTCTTTTC	7378

Db 220 TTGAACGATAGCCTTCTTCTTATCGCAATGATGGCAATTTGTAGAAGCCATCTCTCTTTTC 161

QY 7379 TACTGTCTTTTCGATGAAGTGACAGATAGCTGGCAATGGAATCCGAGGAGGTTTCCCGA 7438

Db 160 TACTGTCTTTTCGATGAAGTGACAGATAGCTGGCAATGGAATCCGAGGAGGTTTCCCGA 101

QY 7439 TATTACCCCTTTGTTGAAGAGTCTCAATAGCCCTCTGGTCTCTCTGAGACTGTATCTTTGAT 7498

Db 100 TATTACCCCTTTGTTGAAGAGTCTCAATAGCCCTCTGGTCTCTCTGAGACTGTATCTTTGAT 41

QY 7499 ATTCTTTGGAGTAGACGAGAGTGTCTGCTCCACCATTGTTG 7538

Db 40 ATCTTTGGAGTAGACGAGAGTGTCTGCTCCACCATTGTTG 1

RESULT 7

ADL71845

ID ADL71845 standard; DNA; 1235 BP.

XX AC ADL71845;

XX DT 20-MAY-2004 (first entry)

XX Arabidopsis thaliana OBP3 antisense DNA #6.

XX Transgenic plant; Dof transcription factor; ocs binding factor;

KW plant size; plant stature; root growth; plant; gene; db; OBP;

KW OBF binding protein; OBP3; SOB1; mouse-ear cress.

XX Arabidopsis thaliana.

XX US2004045055-A1.

PN 04-MAR-2004.

XX 28-AUG-2003; 2003US-00650249.

XX 28-AUG-2002; 2002US-0406657P.

PR (UNIW) UNIV WASHINGTON.

XX Neff MM;

XX WPI; 2004-225757/21.

XX New transgenic plant cell, useful in producing plants with altered size and stature and with normal and healthy root growth.

PS Claim 37; SEQ ID NO 17; 53pp; English.

XX The invention relates to a transgenic plant transformed by a Dof

CC transcription factor, OBF (ocs binding factor) binding protein (OBP3).

CC OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic

CC acid and polypeptides are useful in producing transgenic plants with

CC altered size and stature and with normal and healthy root growth. The

CC present sequence is Arabidopsis thaliana OBP3 antisense DNA.

XX SQ Sequence 1235 BP; 408 A; 222 C; 179 G; 426 T; 0 U; 0 Other;

Query Match 16.3%; Score 1235; DB 12; Length 1235;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3045 CAACCAAGAACGATGACGTATGATTGACTTGCAGAAATAAGCAAAACAAATACCTGTT 3104

Db 1 CAACCAAGAACGATGACGTATGATTGACTTGCAGAAATAAGCAAAACAAATACCTGTT 60

QY 3105 CAAATCGACACTTAATTCGAAAAGGTTAGTAATAGTAAGAGGCTTTTATTATGAAA 3164

Db 61 CAAATCGACACTTAATTCGAAAAGGTTAGTAATAGTAAGAGGCTTTTATTATGAAA 120

QY 3165 ACAAAGAAATAAGAGCCTTAGAGAATGATGAAATTTGAAAGAGAAAAAGAGCATTTG 3224

Db 121 ACAAAGAAATAAGAGCCTTAGAGAATGATGAAATTTGAAAGAGAAAAAGAGCATTTG 180

QY 3225 TTATAGAAAAGAAAAAGAGAGAGTAAAGAGAAATTAAGAAACACAATAAATTAACAA 3284

Db 181 TTATAGAAAAGAAAAAGAGAGAGTAAAGAGAAATTAAGAAACACAATAAATTAACAA 240

QY 3285 AGGAAACTTCATTTCTCTCTTTATCCCAATTCAGCTCCCTCCCTCTCTCTCTCTCTCT 3344

Db 241 AGGAAACTTCATTTCTCTCTTTATCCCAATTCAGCTCCCTCCCTCTCTCTCTCTCTCT 300

QY 3345 CTCTCTCTCTAGATCAATTTCTTTCTTATGATGATGATGATGATGATGATGATGATGATG 3404

Db 301 CTCTCTCTCTAGATCAATTTCTTTCTTATGATGATGATGATGATGATGATGATGATGATG 360

QY 3405 TCTTACCTAAAAAGGATCAAGTAAGAGATTCAAGAGATGATGATGATGATGATGATGATGATG 3464

Db 361 TCTTACCTAAAAAGGATCAAGTAAGAGATTCAAGAGATGATGATGATGATGATGATGATGATG 420

QY 3465 AATCAGTTTCGATTCCTCCCAATTTGGCAGCAGGTAAAGATCAGTTTATGATGATGATGATG 3524

Db 421 AATCAGTTTCGATTCCTCCCAATTTGGCAGCAGGTAAAGATCAGTTTATGATGATGATGATG 480

QY 3525 GTTCTCTGATTCGTTCTCTTTCTCTCAAGCTCGATCAAGATTTATGAAAAATTTGATGAGA 3584

Db 481 GTTCTCTGATTCGTTCTCTTTCTCTCAAGCTCGATCAAGATTTATGAAAAATTTGATGAGA 540

QY 3585 TTTTGTTCGACAAAATTCCTAGCTATTGTGGACGCGCATATATATPACTTATGAATATTC 3644

Db 541 TTTTGTTCGACAAAATTCCTAGCTATTGTGGACGCGCATATATATPACTTATGAATATTC 600

QY 3645 TTAGTTGATTAACCCCTTTTCTTCTCTCTCGAATATACGAAATATATATGAAT 3704

Db 601 TTAGTTGATTAACCCCTTTTCTTCTCTCTCGAATATACGAAATATATATGAAT 660

QY 3705 GATTTCAATTTTGGTCTTTTCTTCTTCTCAAGACTTTTAAAAAATTTATCTTAGTTGA 3764

Db 661 GATTTCAATTTTGGTCTTTTCTTCTTCTCAAGACTTTTAAAAAATTTATCTTAGTTGA 720

QY 3765 TAAAAACCTTTTCTTGTCTCTCAAGGGCTTATGATATAATGTTTCTTACAGGATT 3824

Db 721 TAAAAACCTTTTCTTGTCTCTCAAGGGCTTATGATATAATGTTTCTTACAGGATT 780

QY 3825 AATTTTCTCTTGGTTAGATTTTACACCGCATGGAATATACCTTCAAAAATAAAAA 3884

Db 781 AATTTTCTCTTGGTTAGATTTTACACCGCATGGAATATACCTTCAAAAATAAAAA 840

QY 3885 GTTTAAAGTTACTATGACTTTTAAATCTGAGTTTATTTATCCATTTTCTTTTTCGAGCTTTGT 3944

Db 841 GTTTAAAGTTACTATGACTTTTAAATCTGAGTTTATTTATCCATTTTCTTTTTCGAGCTTTGT 900

QY 3945 TGA AAAA ACTATATAATTAATCTGCAATTTCTTGTCAAAGTAGTCAAAATTTTATCTATTTTC 4004

Db 901 TGA AAAA ACTATATAATTAATCTGCAATTTCTTGTCAAAGTAGTCAAAATTTTATCTATTTTC 960

QY 4005 TTTTGTCTCCGACCAATGTTTCAAACTCGAATCTCTTTCGTTAAAGTTGTTTCTGCTTTA 4064

Db 961 TTTTGTCTCCGACCAATGTTTCAAACTCGAATCTCTTTCGTTAAAGTTGTTTCTGCTTTA 1020

QY 4065 TTATAAACTGAAACTTAATTTAGTACAAATTTATGTTAAATGATGAGCAAGGGAACCAACATC 4124

Db 1021 TTATAAACTGAAACTTAATTTAGTACAAATTTATGTTAAATGATGAGCAAGGGAACCAACATC 1080

QY 4125 AGCTAGAATGTGTCAAACTGACCAAGACCCCTTAATAATTTACTTCGCGAGCTCTCATCAC 4184

Db 1081 AGCTAGAATGTGTCAAACTGACCAAGACCCCTTAATAATTTACTTCGCGAGCTCTCATCAC 1140

QY 4185 CACCGACTTCTCAGTTGCGAGTTTCGAGTCAAGCTAGAGTGAATTCATTTGGTGGACGCTG 4244

Db 1141 CACCGACTTCTCAGTTGCGAGTTTCGAGTCAAGCTAGAGTGAATTCATTTGGTGGACGCTG 1200

QY 4245 CTCGGATCGCAAAAGTCCCATTTGCTGAGCAGCT 4279

Db 1201 CTCGGATCGCAAAAGTCCCATTTGCTGAGCAGCT 1235

QY 4232 ATGTTGGAACGTGCTCGGATCGCAAAAGTCCCATTTGCTGAGCAGCTCTAAATTTGCCCT 4291
Db 1 ATGTTGGAACGTGCTCGGATCGCAAAAGTCCCATTTGCTGAGCAGCTCTAAATTTGCCCT 60
QY 4292 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTTCAATACTATAGCCTTACTCAACT 4351
Db 61 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTTCAATACTATAGCCTTACTCAACT 120
QY 4352 CGCCATTTTGC AAAACAATGTCGTGCTATTTGGAACGCTGGCGGTTCTTGAAGAAATGTT 4411
Db 121 CGCCATTTTGC AAAACAATGTCGTGCTATTTGGAACGCTGGCGGTTCTTGAAGAAATGTT 180
QY 4412 CTTGTTGAGGAGGCTTTAGGAGGAACAAGAGAAGCAATCCAGATCGAAATCTACGGTC 4471
Db 181 CTTGTTGAGGAGGCTTTAGGAGGAACAAGAGAAGCAATCCAGATCGAAATCTACGGTC 240
QY 4472 GTGGTCTCGACTGATAATACTACTAGTACTTCACTCACTTACTTCTCGCCCAAGTTACTCA 4531
Db 241 GTGGTCTCGACTGATAATACTACTAGTACTTCACTCACTTACTTCTCGCCCAAGTTACTCA 300
QY 4532 AACCTTAGCAAGTTTCATAGTACGGTCAAAATCCCGAGTTTAAATTCGAATCTGCCCATC 4591
Db 301 AACCTTAGCAAGTTTCATAGTACGGTCAAAATCCCGAGTTTAAATTCGAATCTGCCCATC 360
QY 4592 TTGCTCTCTCAAAAGCCTTGGAGTTACAAATTCAGCAACACACTGGATTAGATTTTGGT 4651
Db 361 TTGCTCTCTCAAAAGCCTTGGAGTTACAAATTCAGCAACACACTGGATTAGATTTTGGT 420
QY 4652 GGAATCTCAAAATAGCAACATGATAGTGTATGAGTTCTAGTGGTGGGATCTTTGGATGCA 4711
Db 421 GGAATCTCAAAATAGCAACATGATAGTGTATGAGTTCTAGTGGTGGGATCTTTGGATGCA 480
QY 4712 TGGAGAATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACACTACCGGA 4771
Db 481 TGGAGAATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACACTACCGGA 540
QY 4772 TTGGTGCAATCTTCAAAACGCTTATATCCATTTACTAGAGGTAAAGGAGGTGTTAATCAA 4831
Db 541 TTGGTGCAATCTTCAAAACGCTTATATCCATTTACTAGAGGTAAAGGAGGTGTTAATCAA 600
QY 4832 GGTGATTTCTCAACAGAGAGTGTAGTATTTCCATCAGCTAATGTTTAAAGCCTTTGATG 4891
Db 601 GGTGATTTCTCAACAGAGAGTGTAGTATTTCCATCAGCTAATGTTTAAAGCCTTTGATG 660
QY 4892 GATTTTTCTTCAGCGGGGTTAGCGCCAACGCAAAAGAAATGTGAAGCGGGAAGAGAAAT 4951
Db 661 GATTTTTCTTCAGCGGGGTTAGCGCCAACGCAAAAGAAATGTGAAGCGGGAAGAGAAAT 720
QY 4952 GATCAGGATCGGGTAGGATGGGATGGGATGGGATGAATACTTATCAAGAACTTTTGGGT 5011
Db 721 GATCAGGATCGGGTAGGATGGGATGGGATGGGATGAATACTTATCAAGAACTTTTGGGT 780
QY 5012 AATATCAACATAAATCAGCAGGAACAGGGAATACACATCATGGGAGGTAAACAGTTCT 5071
Db 781 AATATCAACATAAATCAGCAGGAACAGGGAATACACATCATGGGAGGTAAACAGTTCT 840
QY 5072 TGGACCGGTTTCACTCCAACTCAACACTCAACAGGCAATCTCTCAATCTAA 5119
Db 841 TGGACCGGTTTCACTCCAACTCAACACTCAACAGGCAATCTCTCAATCTAA 888

RESULT 11

ADL71843

ID ADL71843 standard; DNA; 684 BP.

XX AC ADL71843;

XX AC ADL71843;

XX 20-MAY-2004 (first entry)

XX Arabidopsis thaliana OBP3 antisense DNA #4.

XX Transgenic plant; Dof transcription factor; ocs binding factor;
XX plant size; plant stature; root growth; plant; gene; ds; OBF;
KW
KW

KW OBF binding protein; OBP3; SOB1; mouse-ear cress.

XX Arabidopsis thaliana.

OS US2004045055-A1.

XX 04-MAR-2004.

XX 28-AUG-2003; 2003US-00650249.

XX 28-AUG-2002; 2002US-0406657P.

XX (UNIW) UNIV WASHINGTON.

XX Neff MM;

XX WPI; 2004-225757/21.

XX New transgenic plant cell, useful in producing plants with altered size
XX and stature and with normal and healthy root growth.

XX Claim 29; SEQ ID NO 15; 53pp; English.

XX The invention relates to a transgenic plant transformed by a Dof

XX transcription factor, OBF (ocs binding factor) binding protein (OBP3).

XX OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic

XX acid and polypeptides are useful in producing transgenic plants with

XX altered size and stature and with normal and healthy root growth. The

XX present sequence is Arabidopsis thaliana OBP3 antisense DNA.

XX Sequence 684 BP; 212 A; 145 C; 149 G; 178 T; 0 U; 0 Other;

SQ Query Match 9.0%; Score 684; DB 12; Length 684;

Best Local Similarity 100.0%; Pred. No. 6.2e-195; Indels 0; Gaps 0;

Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4436 AACAGAGAGCAAAATCCAGATCGAAATCTACGGTCTGCTGCTCGACTGATAATACTACT 4495

Db 1 AACAGAGAGCAAAATCCAGATCGAAATCTACGGTCTGCTGCTCGACTGATAATACTACT 60

QY 4496 AGTACTTCACTACTTCTCGCCCAAGTTACTCTAAACCTTAGCAAGTTTCATAGCTAC 4555

Db 61 AGTACTTCACTACTTCTCGCCCAAGTTACTCTAAACCTTAGCAAGTTTCATAGCTAC 120

QY 4556 GGTCAATCCCGAGGTTTAAATTCCAACTTGCCTCTCTCCAAAGCCTTGA 4615

Db 121 GGTCAATCCCGAGGTTTAAATTCCAACTTGCCTCTCTCCAAAGCCTTGA 180

QY 4616 GATTACAATTCAGCAACACTCGATTTAGATTTTGGTGGAACTCAAATAAGCAACATGATA 4675

Db 181 GATTACAATTCAGCAACACTCGATTTAGATTTTGGTGGAACTCAAATAAGCAACATGATA 240

QY 4676 AGTGGTATGAGTTCTAGTGGTGGGATCTTGGATGATGAGAAATACCTCATCAACAA 4735

Db 241 AGTGGTATGAGTTCTAGTGGTGGGATCTTGGATGATGAGAAATACCTCATCAACAA 300

QY 4736 GCTCAGCAATTCCTTTCTTGATCAACACTACCGGATTTGGTGGAACTCAAACGCTTGA 4795

Db 301 GCTCAGCAATTCCTTTCTTGATCAACACTACCGGATTTGGTGGAACTCAAACGCTTGA 360

QY 4796 TATCAATTAAGAAGGTAAAGGAGGTGTTAATCAAGGTGATTCTCAACAGAGAGTAGT 4855

Db 361 TATCAATTAAGAAGGTAAAGGAGGTGTTAATCAAGGTGATTCTCAACAGAGAGTAGT 420

QY 4856 GATTATTCGAATCAGCTAATGTTTAAAGCCTTGTAGGATTTTCTCAGCGGGGTAGG 4915

Db 421 GATTATTCGAATCAGCTAATGTTTAAAGCCTTGTAGGATTTTCTCAGCGGGGTAGG 480

QY 4916 GCCACGCAACAGAAATGTGAAGCGGAAGAGATGATCAGATCGGGGTAGGATGGG 4975

Db 481 GCCACGCAACAGAAATGTGAAGCGGAAGAGATGATCAGATCGGGGTAGGATGGG 540

QY 4976 GATGGAGTGAATAACTTATCAAGAACTTTTGGGTAAATATCAACATAAACTCAGGAGG 5035

PI Broun PE;
XX WPI; 2003-248221/24.
DR P-PSDB; ADD30378.
XX
PT New plant transcription factor polynucleotides and polypeptides, useful
PT in producing transgenic plants with commercially valuable properties,
PT such as an alteration in a plant growth characteristic, e.g. growth rate
PT or apomixis.
XX
XX Disclosure; SEQ ID NO 406; 454pp; English.
PS
XX The invention relates to a number of isolated Arabidopsis thaliana cDNA
XX sequences and their encoded proteins which are especially transcription
CC factor related cDNA's and proteins. The isolated or recombinant plant
CC transcription factor polynucleotides and polypeptides are useful in
CC producing transgenic plants with commercially valuable properties, i.e.
CC modified or altered desirable traits as compared to a reference plant,
CC such as an alteration in a plant growth characteristic, e.g. growth rate,
CC germination rate of seeds, vigor of plants and seedlings, or leaf and
CC flower senescence. Sequence information related to the polynucleotides
CC and polypeptides can also be used in bioinformatic search methods. The
CC transgenic plant is useful for growing a progeny plant from a parent
CC plant. This sequence represents one of the cDNAs of the invention.
XX
SQ Sequence 795 BP; 236 A; 180 C; 175 G; 204 T; 0 U; 0 Other;

Query Match 7.7%; Score 581; DB 10; Length 795;
Best Local Similarity 100.0%; Pred. No. 3.5e-164;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4232 ATGGTGGAAAGCTGCTCGGATCGCAAAAGTCCCATTCGCTGAAGCAGCTCTAAATGGCCCT 4291
Db 1 ATGGTGGAAAGCTGCTCGGATCGCAAAAGTCCCATTCGCTGAAGCAGCTCTAAATGGCCCT 60

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QY 4412 CTGTTGGAGGAGGCTTTTAGGAGGAAACAAGAGCAAAATCCAGATCGAAATCTACGGTC 4471
Db 181 CTGTTGGAGGAGGCTTTTAGGAGGAAACAAGAGCAAAATCCAGATCGAAATCTACGGTC 240

QY 4472 GTGGTCTCGACTGATTAATCTACTAGTCTTCTATCTACTTCTCGCCCAAGTTACTCA 4531
Db 241 GTGGTCTCGACTGATTAATCTACTAGTCTTCTATCTACTTCTCGCCCAAGTTACTCA 300

QY 4532 AACCTTAGCAAGTTTTCATAGCTACGGTCAAAATCCCGAGTTTAAATTCCAACTTGGCCATC 4591
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QY 4712 TGAGAAATACCTCCATCACAAAGCTCAGCAATTCCTTTTCTTGATCAACACTACCGGA 4771
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ADI44304
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AC ADI44304;
XX
DT 22-APR-2004 (first entry)
XX
DE Plant transcription factor related polynucleotide #1741.
XX
KW transgenic; plant; enhanced tolerance to abiotic stress;
KW glyphosphate tolerance; hormone sensitivity; disease resistance;
KW sugar sensing; flowering; flower structure; stem bifurcation;
KW branching pattern; apical dominance; trichome; stem morphology;
KW root growth; root hair; seed development; cell proliferation;
KW cell differentiation; premature senescence; necrosis; plant size;
KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
KW plant anthocyanin; light response; shade avoidance; bioinformatic;
KW transcription factor; ds.
XX
OS Unidentified.
XX
FN US2004019927-A1.
XX
PD 29-JAN-2004.
XX
PF 25-FEB-2003; 2003US-00374780.
XX
PR 18-APR-2001; 2001US-00837944.
XX
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAR/) HAANG V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (DUBE/) PILGRIM M L.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
XX
PI Sherman BK, Riechmann JB, Jiang C, Heard JE, Haake V;
PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;
PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
XX
DR WPI: 2004-132245/13.
XX P-PSDB; ADI44305.
XX
XX New transgenic plant comprising a recombinant polynucleotide of any one
PT of more than 500 nucleotide sequences, useful in bioinformatic search
PT methods.
XX
XX Disclosure; SEQ ID NO 2767; 435pp; English.
XX
XX The invention describes a transgenic plant comprising a recombinant
CC polynucleotide of any one of more than 500 nucleotide sequences fully
CC defined in the specification or its complement. The method of the
CC invention can be used to produce a plant having altered traits such as:
CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone
CC sensitivity; disease resistance; sugar sensing; early or late flowering;
CC altered flower structure, change in stem bifurcations, altered branching
CC pattern, reduced apical dominance, reduced trichome density; lack of
CC trichomes; reduced ectopic trichome development; altered trichome
CC development; increase in trichome number; altered stem morphology;
CC increased root growth; increased root hairs; altered seed development;
CC altered cell proliferation or cell differentiation; rapid development;
CC premature senescence; increased necrosis; increase in seedling or plant
CC size; decreased plant size; leaf morphology; seed morphology; seed
CC biochemistry; increase in root anthocyanins; increase in plant

CC anthocyanins, or alteration in light response or shade avoidance. The
CC transgenic plant, polynucleotides and polypeptides are useful in
CC bioinformatic search methods. This sequence represents a plant
CC transcription factor related polynucleotide.

XX SQ Sequence 795 BP; 236 A; 180 C; 175 G; 204 T; 0 U; 0 Other;

Query Match 7.7%; Score 581; DB 12; Length 795;
Best Local Similarity 100.0%; Pred. No. 3.5e-164;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4232 ATGGTGGAAAGTCTCGGATCGCAAAAGTCCCAATTCGCTGAAGCAGCTCTAAATTCGCCCT 4291
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Db 1 ATGGTGGAAAGTCTCGGATCGCAAAAGTCCCAATTCGCTGAAGCAGCTCTAAATTCGCCCT 60

QY 4292 AGATGTGACTCAACCAATCTAAGTCTCTGTTACTTCAATAAATCTATAGCCCTTACTCAACCT 4351
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Db 61 AGATGTGACTCAACCAATCTAAGTCTCTGTTACTTCAATAAATCTATAGCCCTTACTCAACCT 120

QY 4352 CGCCATTTCTGCAAAACATGTCGCTGCTATTTGACACGTCGGCGGTTCTTTGAGGAATGTT 4411
|||||
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|||||
Db 181 CCTGTTGGAGGAGCTTTAGGAGGACAGAGCAAAATCCAGATCGAAATCTACGCTC 240

QY 4472 GTGGTCTCGACTGATTAATCTACTAGTACTTCTATCTACTTCTCGCCCAAGTTACTCA 4531
|||||
Db 241 GTGGTCTCGACTGATTAATCTACTAGTACTTCTATCTACTTCTCGCCCAAGTTACTCA 300

QY 4532 AACCTTAGCAAGTTTCATAGTACGTCGCTCAAAATCCCGAGTTTAAATTCCAACTTGCCCATC 4591
|||||
Db 301 AACCTTAGCAAGTTTCATAGTACGTCGCTCAAAATCCCGAGTTTAAATTCCAACTTGCCCATC 360

QY 4592 TTGCTCTCTCCAAAGCTTCGAGATTACAAATTCAGCAACACTCGATTAGTTTGGT 4651
|||||
Db 361 TTGCTCTCTCCAAAGCTTCGAGATTACAAATTCAGCAACACTCGATTAGTTTGGT 420

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QY 4712 TGGAGTAATCTCCATCAACAACAGCTCAGCAATTCCTTTCTTGATCAACACTACCGGA 4771
|||||
Db 481 TGGAGTAATCTCCATCAACAACAGCTCAGCAATTCCTTTCTTGATCAACACTACCGGA 540

QY 4772 TTGGTGCATCTTCAACCGGTTATATCCATTACTAGAAGG 4812
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Db 541 TTGGTGCATCTTCAACCGGTTATATCCATTACTAGAAGG 581

RESULT 15

ABX56844

ID ABX56844 standard; DNA; 577 BP.

XX AC ABX56844;

XX DT 20-FEB-2003 (first entry)

XX DE Arabidopsis thaliana polynucleotide #196.

XX KW Thale cress; gene; ds; genetic manipulation; plant; biosynthesis;

XX KW genetic modification; environmental stress; disease resistance;

XX KW fungicide; insecticide; stress tolerance.

XX XX Arabidopsis thaliana.

XX OS US2002040489-A1.

XX PN 04-APR-2002.

XX PD 26-JAN-2001; 2001US-00770152.

XX PF

XX

PR

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27-JAN-2000; 2000US-0178503P.

(GORL/) GORLACH J.

(ANY/) AN Y.

(HAMI/) HAMILTON C M.

(PRIC/) PRICE J L.

(RAIN/) RAINES T M.

(YUY/) YU Y.

(PAGE/) PAGE A.

(MATH/) MATHW A V.

(LEDE/) LEDFORD B L.

(WOES/) WOESSNER J P.

(HAAS/) HAAS W D.

(GARC/) GARCIA C A.

(KRIC/) KRICKER M.

(SLAT/) SLATER T.

(DAVI/) DAVIS K R.

(ALLE/) ALLEN K.

(HOFF/) HOFFMAN N.

(HURB/) HURBAN P.

WPI; 2003-110410/10.

Novel Arabidopsis thaliana nucleic acid useful for identifying homologous

or related genes, and to create genetically modified and transgenic

organisms, such as plant cells and plants.

Claim 1; SEQ ID NO 196; 45pp; English.

The invention relates to Arabidopsis thaliana nucleic acid sequences. The

DNA sequences and the polypeptides they encode are useful for identifying

homologous or related genes, for producing compositions that modulate the

expression or function of the polypeptides, for mapping functional

regions of the protein, in diagnosis, for studying associated

physiological pathways, for genetic manipulation of cells, preferably

plant cells, in screening assays of various plant strains to determine

the strains that are capable of withstanding a particular disease or

environmental stress, for enhancing or inhibiting production of

biosynthetic products in plants and to create genetically modified and

transgenic organisms, such as plant cells and plants. Transgenic plants

are useful for introducing or improving disease resistance and stress

tolerance in plants, screening biologically active agents, such as

fungicides and insecticides, and for elucidating biochemical pathways.

Sequences ABX56649-ABX57647 represent Arabidopsis thaliana

polynucleotides of the invention. Note: The sequence data for this patent

did not form part of the printed specification but was obtained in

electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 577 BP; 169 A; 80 C; 137 G; 191 T; 0 U; 0 Other;

Query Match 7.6%; Score 577; DB 10; Length 577;

Best Local Similarity 100.0%; Pred. No. 5.9e-163;

Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CAAGAAATGTGAAGCGGGAAGAGATGATCAGGATCGGGGTAGGGATGGAGTGA 60

QY 4986 ATAACCTATCAAGAACTTTTGGGTATATCAATCAACTCAGCAGACGAGGAAT 5045

Db 61 ATAACCTATCAAGAACTTTTGGGTATATCAATCAACTCAGCAGACGAGGAAT 120

QY 5046 ACACATCATGGGAGGTAAACAGTTCTTGGACCGGTTTACCTCCCAACACTCAACAGGCC 5105

Db 121 ACACATCATGGGAGGTAAACAGTTCTTGGACCGGTTTACCTCCCAACACTCAACAGGCC 180

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0

Searched: 5881141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 9: gb_ro.*
- 10: gb_sts.*
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- 13: gb_vl.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	703	9.3	1274	15	AF155818
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9	332	4.4	4462	11	VFO551314
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C 24	300	4.0	552	6	AX405124	AX405124 Sequence
C 25	299	3.9	323	6	AR643977	AR643977 Sequence
C 26	299	3.9	323	6	AX044091	AX044091 Sequence
C 27	222	2.9	470	6	AR437667	AR437667 Sequence
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C 30	222	2.9	711	11	ARPT100	X05868 Plasmid pRT
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C 34	222	2.9	6500	6	BD209863	BD209863 Improved
C 35	222	2.9	6750	6	BD209861	BD209861 Improved
C 36	222	2.9	7074	6	BD209860	BD209860 Improved
C 37	222	2.9	10100	6	BD209864	BD209864 Improved
C 38	222	2.9	10100	6	BD209864	BD209864 Improved
C 39	222	2.9	10166	6	BD209867	BD209867 Improved
C 40	222	2.9	10166	6	BD209867	BD209867 Improved
C 41	222	2.9	10240	6	BD209865	BD209865 Improved
C 42	222	2.9	10272	6	BD209866	BD209866 Improved
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C 44	222	2.9	14446	6	AX275255	AX275255 Sequence
C 45	221	2.9	2728	6	A51131	A51131 Sequence 7

ALIGNMENTS

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DEFINITION	Arabidopsis thaliana (thale cress)				
ACCESSION	AL132975				
VERSION	AL132975.1				GI:6434228
KEYWORDS	Arabidopsis thaliana				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi				
REFERENCE	1	Benes, V., Wurmbach, E., Drzonek, H., Ansorge, W., Mewes, H. W., Lemcke, K., Mayer, K. F. X., Quetier, F. and Salanoubat, M.			
AUTHORS	Unpublished				
JOURNAL	2	(bases 1 to 103240)			
REFERENCE	EU Arabidopsis sequencing project.				
AUTHORS	Submitted (23-FEB-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemckemips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue Gaston Crémieux, BP191, 91006 Evry Cedex, France;				
TITLE	http://www.genoscope.cns.fr				
JOURNAL	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/chal/.				
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SOURCE	Activation-tagging vector pSKI015		
ORGANISM	other sequences; artificial sequences; vectors.		
REFERENCE	1 (bases 1 to 10138)		
AUTHORS	Weigel,D., Ahn,J.H., Blazquez,M.A., Borevitz,J.O., Christensen,S.K., Fankhauser,C., Ferrandiz,C., Kardailsky,I., Malancharuvill,E.J., Neff,M.M., Nguyen,J.T., Sato,S., Wang,Z., Xia,Y., Dixon,R.A., Harrison,M.J., Lamb,C.J., Yanofsky,M.P. and Chory,J.		
TITLE	Activation tagging in Arabidopsis		
JOURNAL	Plant Physiol. 122 (4), 1003-1013 (2000)		
PUBLISHED	10759496		
REFERENCE	2 (bases 1 to 10138)		
AUTHORS	Kardailsky,I. and Weigel,D.		
TITLE	Direct Submision		
JOURNAL	Submitted (17-SEP-1999) Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
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ACCESSION AF218466
VERSION AF218466.1 GI:6715465
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SOURCE Activation tagging vector pSKI074
ORGANISM Activation tagging vector pSKI074
REFERENCE 1 (bases 1 to 10450)
AUTHORS Weigel,D., Ahn,J.H., Blazquez,M.A., Borevitz,J.O.,
Christensen,S.K., Fankhauser,C., Ferrandiz,C., Kardailsky,I.,
Malancharuvil,B.J., Neff,M.M., Nguyen,J.T., Sato,S., Wang,Z.,
Xia,Y., Dixon,R.A., Harrison,M.J., Lamb,C.J., Yanofsky,M.F. and
Chory,J.

TITLE Activation tagging in Arabidopsis
JOURNAL Plant Physiol. 122 (4), 1003-1013 (2000)
PUBMED 10759496
REFERENCE 2 (bases 1 to 10450)
AUTHORS Weigel,D., Blazquez,M.A., Borevitz,J., Christensen,S.K.,
Fankhauser,C., Ferrandiz,C., Malancharuvil,B.J., Neff,M.M.,
Nguyen,J.T., Sato,S., Xia,Y., Wang,Z., Dixon,R.A., Harrison,M.J.,
Lamb,C.J., Yanofsky,M.F. and Chory,J.

Direct Submission
Submitted (22-DEC-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA

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DEFINITION	Arabidopsis thaliana zinc finger protein OBP3 mRNA, complete cds.		
ACCESSION	AF155818		
VERSION	AF155818.1	GI:5059397	
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SOURCE	Arabidopsis thaliana		
ORGANISM	Arabidopsis thaliana		
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REFERENCE	1 (bases 1 to 1274)		
AUTHORS	Kang,H.G. and Singh,K.B.		
TITLE	Characterization of Arabidopsis Dof Transcription Factors, a Novel Zinc Finger Protein Family in Plants		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1274)		
AUTHORS	Kang,H.G. and Singh,K.B.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-JUN-1999) MCDB, University of California, Los Angeles, 405 Hilgard Ave., Los Angeles, CA 90095, USA		
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	/translation="MVVERARIAKVLPEAALNCPKDSNTKFCYFNYSLTQPRHFC KTCRRYWTGGSLRNVPGGFRNKRKSKSVTVVSDTNTSTSLTSPSYSNP SXFHSYGIQPFNSNLPILPQISGIDNSNIGLDFGTQISNIMSGSGGILDA WRIPPSQAOQPFLLINTTGLVOSSNALYPLLEGGVSATQTRNVKAEENDQDRGRDGD GVNILSRNPLGNINISGRNEEYTSWGGNSWTGFTSNNSTGHLSP"		
ORIGIN			
Query Match	9.3%; Score 703; DB 15; Length 1274;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 703; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	4110	AAGGGAAACCAACATCAGCTAGATGTGTACACTGACAGAACCCCTAATATTACTTAC	4169
Db	16	AAGGGAAACCAACATCAGCTAGATGTGTACACTGACAGAACCCCTAATATTACTTAC	75
QY	4170	GGCAGCTCTCATCACACCGACTTCTCAGGTTGCGAGTTCGAGTCAAGCTAGAGTCAAT	4229
Db	76	GGCAGCTCTCATCACACCGACTTCTCAGGTTGCGAGTTCGAGTCAAGCTAGAGTCAAT	135
QY	4230	CAATGTGGAACTGCTCGAGTCGAAAGTCATTCGCTGACAGCTCTAAATGGC	4289
Db	136	CAATGTGGAACTGCTCGAGTCGAAAGTCATTCGCTGACAGCTCTAAATGGC	195
QY	4290	CTAGATGTGACTCAACCAATCTTCTGTTTACTTCAATACTACTAGCTTACTCAAC	4349
Db	196	CTAGATGTGACTCAACCAATCTTCTGTTTACTTCAATACTACTAGCTTACTCAAC	255

QY	4350	CTCGCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTGGCGGTCTCTTCAGGAATG	4409
Db	256	CTCGCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTGGCGGTCTCTTCAGGAATG	315
QY	4410	TTCTGTTGGAGAGGCTTTTAGGAGGAACAAGAGCAAAATCCAGATCGAAATCTACGG	4469
Db	316	TTCTGTTGGAGAGGCTTTTAGGAGGAACAAGAGCAAAATCCAGATCGAAATCTACGG	375
QY	4470	TGTTGGTCTCGACTGATTAATCTAGTACTTTCATCTACTTCTTCGCCCCAAGTTACT	4529
Db	376	TGTTGGTCTCGACTGATTAATCTAGTACTTTCATCTACTTCTTCGCCCCAAGTTACT	435
QY	4530	CAAAACCTAGCAAGTTTCATAGCTACGGTCAAAATCCCGAGTTTAATTCCAACTTGCCTCA	4589
Db	436	CAAAACCTAGCAAGTTTCATAGCTACGGTCAAAATCCCGAGTTTAATTCCAACTTGCCTCA	495
QY	4590	TCTTGCTCTCTCTCCAAAGCCTTGGAGATTACAATTCAAAGCAACACTGGATTAGATTTTG	4649
Db	496	TCTTGCTCTCTCTCCAAAGCCTTGGAGATTACAATTCAAAGCAACACTGGATTAGATTTTG	555
QY	4650	GTGGAACTCAATATAGCAACATGATAGTGGTATGATGTTCTAGTGTGGATCTTGGATG	4709
Db	556	GTGGAACTCAATATAGCAACATGATAGTGGTATGATGTTCTAGTGTGGATCTTGGATG	615
QY	4710	CATGGAGTACTCTCCATCACCAAGCTCAGCAATTCCTCTTCTTGATCAACACTACCG	4769
Db	616	CATGGAGTACTCTCCATCACCAAGCTCAGCAATTCCTCTTCTTGATCAACACTACCG	675
QY	4770	GATTGGTCAATCTTCCAAACGGGTATATCCATTACTAGAAGG	4812
Db	676	GATTGGTCAATCTTCCAAACGGGTATATCCATTACTAGAAGG	718
RESULT 6			
AX508868			
LOCUS	AX508868	2000 bp	DNA linear PAT 27-SEP-2002
DEFINITION	Sequence 3563 from Patent WO216655.		
ACCESSION	AX508868		
VERSION	AX508868.1	GI:23390105	
KEYWORDS	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE	1		
AUTHORS	Harper,J.F., Krebs,J., Wang,X. and Zhu,T.		
TITLE	Stress-regulated genes of plants, transgenic plants containing same, and methods of use		
JOURNAL	Patent: WO 0216655-A 3563 28-FEB-2002; The Scripps Research Institute (US) ; Syngenta Participations AG (CH)		
FEATURES	Location/Qualifiers		
Source	1..2000		
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	/mol_type="unassigned DNA"		
	/db_xref="taxon:3702"		
ORIGIN			
Query Match	4.9%; Score 368; DB 6; Length 2000;		
Best Local Similarity	100.0%; Pred. No. 3e-155;		
Matches 368; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	5763	GAATTATGCACTTAATTCAGACTAATCCCCCAAAATTCAGAAATTTATGATTTTTCG	5822
Db	1	GAATTATGCACTTAATTCAGACTAATCCCCCAAAATTCAGAAATTTATGATTTTTCG	60
QY	5823	ATTTAATATTGTTCACAATCATATATGCGCAACTAACTTAATTGAAAGACAATGAATG	5882
Db	61	ATTTAATATTGTTCACAATCATATATGCGCAACTAACTTAATTGAAAGACAATGAATG	120
QY	5883	ACTGAAACCATGCATTAATCTCTCAAGTCTCAACCTATGAAGATCATGTAACCAATAGAC	5942

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Db 121 ACTGAACCATGATAATCTCTCAAGTCTCAACCTATGAAGAATCATGTAAACCAATAGAC 180
QY 5943 TATCATCATGATTAGTAAATGATGATCTATAATGTAATCTTTTGACATAGATATGTCAT 6002
Db 181 TATCATCATGATTAGTAAATGATGATCTATAATGTAATCTTTTGACATAGATATGTCAT 240
QY 6003 TTATCTGGATATAAAGATGGCGTTTAACTCTACTTTTGGCAATTTTGTGTATATCTTTCTTC 6062
Db 241 TTATCTGGATATAAAGATGGCGTTTAACTCTACTTTTGGCAATTTTGTGTATATCTTTCTTC 300
QY 6063 TAATACATATGATCAATACACTTTTGTGTTTTTAAAGAAATTAATAAATTTATTTCAAACAT 6122
Db 301 TAATACATATGATCAATACACTTTTGTGTTTTTAAAGAAATTAATAAATTTATTTCAAACAT 360
QY 6123 CGATCACA 6130
Db 361 CGATCACA 368

RESULT 7
AB017485/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Nicotiana tabacum (common tobacco)
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 2939)
Yamada,T., Tanaka,Y. and Kasumi,T.
Putative negative regulator for plant apoptosis
Published Only in DataBase (1999)
REFERENCE
2 (bases 1 to 2939)
Yamada,T., Tanaka,Y. and Kasumi,T.
Direct Submission
Submitted (03-SEP-1998) Tetsuji Yamada, Okayama University, Faculty
of Agriculture, Tsushima Naka 1-1, Okayama, Okayama 700-8530, Japan
(E-mail:tdry@cc.okayama-u.ac.jp, Tel:81-86-251-8307,
Fax:81-86-251-8307)
FEATURES
source
1..2939
/organism="Nicotiana tabacum"
/mol_type="genomic DNA"
/cultivar="Bright Yellow"
/db_xref="taxon:4097"
/clone="Tentatively names as S-5"
/cell_type="Suspension cultures"
ORIGIN
Query Match 4.8%; Score 362; DB 15; Length 2939;
Best Local Similarity 100.0%; Pred. No. 2,1e-162;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6263 TGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAAACATAGCCTTTCCTTT 6322
Db 364 TGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAAACATAGCCTTTCCTTT 305
QY 6323 ATCGCAATGATGCATTTGAGAGCCATCTTCTTTCTACGTCTTTCGATGAAGTG 6382
Db 304 ATCGCAATGATGCATTTGAGAGCCATCTTCTTTCTACGTCTTTCGATGAAGTG 245
QY 6383 ACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATATACCTTTGTTGAAAAGT 6442
Db 244 ACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATATACCTTTGTTGAAAAGT 185
QY 6443 CTCATAGCCCTCTGGCTTTCTGAGACTGTAATCTTTGATATTTCTGGAGTAGACGAGT 6502
Db 184 CTCATAGCCCTCTGGCTTTCTGAGACTGTAATCTTTGATATTTCTGGAGTAGACGAGT 125
QY 6503 GTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTGTCTTTGAAGACGT 6562
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Db 124 GTGCTGCTCCACCATGTTGGGATCTAGATATCACATCAATCCACTTGTCTTTGAAGACGT 65
QY 6563 GGTTCGGAACGTCTCTTTTCCACCATGTTCTCTGCTGGGTGGGTCCATCTTTTGGGACC 6622
Db 64 GGTTCGGAACGTCTCTTTTCCACCATGTTCTCTGCTGGGTGGGTCCATCTTTTGGGACC 5
QY 6623 AC 6624
Db 4 AC 3

AJ616346 1431 bp DNA linear PLN 01-JUL-2004
Nicotiana tabacum chloroplast kr1 DNA integrant.
AJ616346
AJ616346.1 GI:45724967
SOURCE
Nicotiana tabacum (common tobacco)
ORGANISM
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1
Huang,C.Y., Avliffe,M.A. and Timmis,J.N.
Simple and complex nuclear loci created by newly transferred
chloroplast DNA in tobacco
Proc. Natl. Acad. Sci. U.S.A. 101 (26), 9710-9715 (2004)
15210980
Huang,C.Y.
REFERENCE
2 (bases 1 to 1431)
Direct Submission
Submitted (05-DEC-2003) Huang C.Y., School of Molecular &
Biomedical Science, The University of Adelaide, The University of
Adelaide, South Australia, 5005 Adelaide, AUSTRALIA
Location/Qualifiers
1..1431
/organism="Nicotiana tabacum"
/mol_type="genomic DNA"
/cultivar="Petit Havana (N, N)"
/db_xref="taxon:4097"
/note="kr1 integrant"
misc_feature 1..385
/note="neoTSL2 sequence"
misc_feature 386..451
/note="chloroplast DNA of pPRV111A"
misc_feature 451..452
/note="recombination junction (J1-2)"
misc_feature 452..779
/note="aada sequence of pPRV111A"
misc_feature 729..734
/note="EcoRI site"
misc_feature 780..1431
/note="neoTSL2 sequence"
ORIGIN
Query Match 4.4%; Score 332; DB 15; Length 1431;
Best Local Similarity 100.0%; Pred. No. 6.4e-148;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGTCTTTGAAGACGTGGTGGAACTCTCTTTTCCACGA 6249
Db 1131 AGATATCACATCAATCCACTTGTCTTTGAAGACGTGGTGGAACTCTCTTTTCCACGA 1072
QY 6250 TGTTCCTCTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 6309
Db 1071 TGTTCCTCTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 1012
QY 6310 TAGCCCTTCTTTATCGCAATGATGCAATTTAGAGGCATCTTCTTTCTACTGTCC 6369
Db 1011 TAGCCCTTCTTTATCGCAATGATGCAATTTAGAGGCATCTTCTTTCTACTGTCC 952
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QY 6370 TTTTCGATGAAGTCACAGATAGCTGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 6429
Db 951 TTTTCGATGAAGTCACAGATAGCTGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 892
QY 6430 TTTTGTGAAAGTCTCAATAGACCTCTGCTCTCTGAGACTGTATCTTTGATATTCTTGG 6489
Db 891 TTTTGTGAAAGTCTCAATAGACCTCTGCTCTCTGAGACTGTATCTTTGATATTCTTGG 832
QY 6490 AGTAGACGAGAGTGTCTGCTCTCCACCATGTTG 6521
Db 831 AGTAGACGAGAGTGTCTGCTCTCCACCATGTTG 800

RESULT 9
VF0551314/c
LOCUS VF0551314 4462 bp DNA circular SYN 27-MAR-2003
DEFINITION Transfection vector pBTdest.
ACCESSION AJ551314
VERSION AJ551314.1 GI:29335742
KEYWORDS amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol
acetyl transferase; control of cell death B protein.
SOURCE Transfection vector pBTdest
ORGANISM Transfection vector pBTdest
other sequences; artificial sequences; vectors.
REFERENCE 1
AUTHORS Jakob,M.J., Heim,M.A. and Weisshaar,B.
TITLE Use of a gateway compatible vector for transient plant transfection
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4462)
AUTHORS Jakob,M.J.
DIRECT SUBMISSION
SUBMITTED (26-MAR-2003) Jakob M.J., Salamini, MPI for Plant
Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY
LOCATION/Qualifiers
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1. 4462
/organism="Transfection vector pBTdest"
/mol_type="other DNA"
/db_xref="taxon:225975"
31..443
/note="35S"
421..424
/note="35S"
456..580
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689..1348
/gene="cat"
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/protein_id="CAD83080.1"
/db_xref="GI:29335743"
/translation="MEKKTITGVTTVDISOWHRKHEFAFQSVACQTYNQTVOLDITAF
LXTVKXKHKFPATPHILARLMAHPRMAKDGELVIMDSVHPCYTVHEQOTFE
SLWSEYHDDPQFQHLIYSQDVACYGENLAYFPKGFENMFVSNPWPVSTFSLNV
ANMDDFFAPVTMGKYTTGQDKVLMPLAIQVHHAHVCDGPHVGRMLNELQQYCDWEQGG
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1690..1995
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1690..1995
/gene="ccdB"
/codon_start=1
/product="control of cell death B protein"
/protein_id="CAD83081.1"
/db_xref="GI:29335744"
/translation="MQFKVYTKRSRYRLFVDVQSDIIDTPGRRMVPIPLASRLISD
KVSRELYPVVHIGDSRWMTMDASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
2036..2160
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gene
terminator
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gene 2606..3466
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/protein_id="CAD83082.1"
/db_xref="GI:29335745"
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DRWEPELNEATPNDERDTTPVMATTLTKLLTGLLTLASRQQLIDMWEADKVAGPL
LRSLAPAGWFIADKSGAGERSGRIIAALGPDGKPSRIWVIVTTGSGATMDERNQIA
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ORIGIN
Query Match 4.4%; Score 332; DB 11; Length 4462;
Best Local Similarity 100.0%; Pred. No. 5.2e-148;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6190 AGATATCACATCAATCCACTTCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 6249
Db 358 AGATATCACATCAATCCACTTCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 299
QY 6250 TGTTCCTCTGTTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 6309
Db 298 TGTTCCTCTGTTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 239
QY 6310 TAGCCTTTCTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTCC 6369
Db 238 TAGCCTTTCTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTTCTACTGTCC 179
QY 6370 TTTTCGATGAAGTCACAGATAGCTGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 6429
Db 178 TTTTCGATGAAGTCACAGATAGCTGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 119
QY 6430 TTTTGTGAAAGTCTCAATAGACCTCTGCTCTCTGAGACTGTATCTTTGATATTCTTGG 6489
Db 118 TTTTGTGAAAGTCTCAATAGACCTCTGCTCTCTGAGACTGTATCTTTGATATTCTTGG 59
QY 6490 AGTAGACGAGAGTGTCTGCTCTCCACCATGTTG 6521
Db 58 AGTAGACGAGAGTGTCTGCTCTCCACCATGTTG 27

RESULT 10
LOCUS AF406991/c 9663 bp DNA linear SYN 13-NOV-2003
DEFINITION Tobacco rattle virus RNA2-based VIGS vector pTRV2, complete
sequence.
ACCESSION AF406991
VERSION AF406991.1 GI:21389151
KEYWORDS Tobacco rattle virus RNA2-based VIGS vector pTRV2 (pYL156)
Tobacco rattle virus RNA2-based VIGS vector pTRV2
SOURCE Tobacco rattle virus RNA2-based VIGS vector pTRV2
ORGANISM Tobacco rattle virus RNA2-based VIGS vector pTRV2
other sequences; artificial sequences; vectors.
REFERENCE 1 (bases 1 to 9663)
AUTHORS Liu,Y., Schiff,M., Marathe,R. and Dinesh-Kumar,S.P.
TITLE Tobacco Rar1, EDS1 and NPR1/NIM1 like genes are required for
N-mediated resistance to tobacco mosaic virus
JOURNAL Plant J. 30 (4), 415-429 (2002)
PUBMED 12028572
REFERENCE 2 (bases 1 to 9663)
AUTHORS Liu,Y.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-2001) MCDB, Yale University, 165 Prospect Street,
New Haven, CT 06520, USA
LOCATION/Qualifiers
1..9663
/organism="Tobacco rattle virus RNA2-based VIGS vector
pTRV2"
/mol_type="other DNA"
/db_xref="taxon:188057"

FEATURES
source
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/note="Tobacco rattle virus RNA2-based T-DNA vector
synonym: pYL156"
1..1639
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1640..1708
/note="multiple cloning site region"
1709..2103
/note="TRV strain ppk20 RNA2 3'-sequence"
2104..2154
/note="synthetic sequence"
2155..2894
/note="pCambia 0390 sequence"
8895..9663
/note="CamV 35S promoter from pCASS2"

ORIGIN
Query Match      4.4%; Score 332; DB 11; Length 9663;
Best Local Similarity 100.0%; Pred. No. 4.5e-148;
Matches 332; Conserved 0; Mismatches 0; Indels 0; Gaps 0;
QY 6190 AGATATCATCAATCCACTTCTGTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 6249
Db 9577 AGATATCATCAATCCACTTCTGTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 9518
QY 6250 TGTTCCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 6309
Db 9517 TGTTCCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 9458
QY 6310 TAGCCCTTCCTTTATCGCAATGATGGCATTTGTGAAGCCATCTTCTCTTTCTACTGTCC 6369
Db 9457 TAGCCCTTCCTTTATCGCAATGATGGCATTTGTGAAGCCATCTTCTCTTTCTACTGTCC 9398
QY 6370 TTTTCGTAAGTGCACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCC 6429
Db 9397 TTTTCGTAAGTGCACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCC 9338
QY 6430 TTTGTTGAAAGTCTCAATAGCCCTCTGTCCTCTGAGACTGTACTTTGATATCTTGG 6489
Db 9337 TTTGTTGAAAGTCTCAATAGCCCTCTGTCCTCTGAGACTGTACTTTGATATCTTGG 9278
QY 6490 AGTAGACGAGAGTGTCTGCTCCACCATTGTTG 6521
Db 9277 AGTAGACGAGAGTGTCTGCTCCACCATTGTTG 9246

RESULT 11
AY788908/c      12537 bp      DNA      circular SYN 02-MAR-2005
LOCUS      N-terminal TAPA T-DNA vector pN-TAPA, complete sequence.
DEFINITION      AY788908
ACCESSION      AY788908
VERSION      AY788908.1 GI:55824365
KEYWORDS      N-terminal TAPA T-DNA vector pN-TAPA
SOURCE      N-terminal TAPA T-DNA vector pN-TAPA
ORGANISM      other sequences; artificial sequences; vectors.
REFERENCE      1 (bases 1 to 12537)
AUTHORS      Rubio,V., Shen,Y., Saijo,Y., Liu,Y., Gusmaroli,G.,
Dinesh-Kumar,S.P. and Deng,X.W.
TITLE      An alternative tandem affinity purification strategy applied to
Arabidopsis protein complex isolation
JOURNAL      Plant J. 41 (5), 767-778 (2005)
PUBMED      15703063
REFERENCE      2 (bases 1 to 12537)
AUTHORS      Rubio,V. and Deng,X.W.
TITLE      Direct Submission
JOURNAL      Submitted (21-OCT-2004) MCDB, Yale University, 165, Prospect St.,
New Haven, CT 06511, USA
FEATURES
source      Location/Qualifiers
            1..12537
            /organism="N-terminal TAPA T-DNA vector pN-TAPA"
            /mol_type="other DNA"
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            /note="derived from pp2p22"
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/note="duplicated CamV 35S promoter"
780..844
/note="TMV U1 omega sequence"
854..1231
/note="2x protein A IgG binding domain"
1256..1279
/note="protease 3C cleavage site"
1286..1303
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1325..1675
/note="9x myc tag"
1704..3577
/note="attR1-CmR-ccdB-attR2 GATEWAY cassette"
3607..3863
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ORIGIN
Query Match      4.4%; Score 332; DB 11; Length 12537;
Best Local Similarity 100.0%; Pred. No. 4.3e-148;
Matches 332; Conserved 0; Mismatches 0; Indels 0; Gaps 0;
QY 6190 AGATATCATCAATCCACTTCTGTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 6249
Db 683 AGATATCATCAATCCACTTCTGTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 624
QY 6250 TGTTCCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 6309
Db 623 TGTTCCTCGTGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 564
QY 6310 TAGCCCTTCCTTTATCGCAATGATGGCATTTGTGAAGCCATCTTCTCTTTCTACTGTCC 6369
Db 563 TAGCCCTTCCTTTATCGCAATGATGGCATTTGTGAAGCCATCTTCTCTTTCTACTGTCC 504
QY 6370 TTTTCGTAAGTGCACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCC 6429
Db 503 TTTTCGTAAGTGCACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTACCC 444
QY 6430 TTTGTTGAAAGTCTCAATAGCCCTCTGTCCTCTGAGACTGTACTTTGATATCTTGG 6489
Db 443 TTTGTTGAAAGTCTCAATAGCCCTCTGTCCTCTGAGACTGTACTTTGATATCTTGG 384
QY 6490 AGTAGACGAGAGTGTCTGCTCCACCATTGTTG 6521
Db 383 AGTAGACGAGAGTGTCTGCTCCACCATTGTTG 352

RESULT 12
AY737283/c      12607 bp      DNA      circular SYN 02-MAR-2005
LOCUS      C-terminal TAP T-DNA vector pYL436, complete sequence.
DEFINITION      AY737283
ACCESSION      AY737283
VERSION      AY737283.1 GI:52630860
KEYWORDS      C-terminal TAP T-DNA vector pYL436
SOURCE      C-terminal TAP T-DNA vector pYL436
ORGANISM      other sequences; artificial sequences; vectors.
REFERENCE      1 (bases 1 to 12607)
AUTHORS      Rubio,V., Shen,Y., Saijo,Y., Liu,Y., Gusmaroli,G.,
Dinesh-Kumar,S.P. and Deng,X.W.
TITLE      An alternative tandem affinity purification strategy applied to
Arabidopsis protein complex isolation
JOURNAL      Plant J. 41 (5), 767-778 (2005)
PUBMED      15703063
REFERENCE      2 (bases 1 to 12607)
AUTHORS      Liu,Y. and Dinesh-Kumar,S.P.
TITLE      A C-terminal tandem affinity purification (TAP) T-DNA vector pYL436
JOURNAL      Unpublished
REFERENCE      3 (bases 1 to 12607)
AUTHORS      Liu,Y. and Dinesh-Kumar,S.P.
TITLE      Direct Submission
JOURNAL      Submitted (28-AUG-2004) MCDB, Yale University, New Haven, CT 06520,
USA
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SOURCE      Binary vector pLH7000
ORGANISM    Binary vector pLH7000
REFERENCE   Other sequences; artificial sequences; vectors.
AUTHORS     Hausmann,L. and Toepfer,R.
TITLE       Development of Plasmid Vectors
JOURNAL     (in) Brauer,D., Roebelen,G. and Toepfer,R. (Eds.);
            BIOENGINEERING OF CUSTOM-TAILED RAPE VARIETIES: 155-172;
            GPZ e. V., Von Sieboldstr. 8, Goettingen, Germany (1999)
REFERENCE   2 (bases 1 to 8911)
AUTHORS     Hausmann,L. and Toepfer,R.
TITLE       Direct Submission
JOURNAL     Submitted (12-FEB-2003) Institute for Grapevine Breeding
            Geilweilerhof, Siebeldingen 76833, Germany
FEATURES   Location/Qualifiers
            1..8911
               /organism="Binary vector pLH7000"
               /mol_type="other DNA"
               /db_xref="taxon:226215"
            6..424
               /note="promoter/enhancer sequence from the 35S gene of
               Cauliflower mosaic virus in GenBank Accession Numbers
               X05868 and V00140"
               360..363
               CAAT_signal
               392..398
               TATA_signal
               misc_feature
               423
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               436..990
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CDS
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DEFINITION Binary vector pLH5000, complete sequence.
ACCESSION AY234327
VERSION AY234327.1 GI:29569706
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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U00613, Tn917 resolvase in GenBank Accession Number
M1180, and RK2 ParA in GenBank Accession Number L27758"
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Query Match 4.4%; Score 331; DB 11; Length 8958;
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6190 AGATATCATCATCAATCCACTTCTTTGAAGACGTGTTGGAACGCTCTTTTTCACGA 6249
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OM nucleic - nucleic search, using sw model

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Searched: 1303057 seqs, 888780828 residues

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Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	281	3.7	4839	3	Sequence 46, Appl
C 3	222	2.9	470	3	Sequence 1, Appl
C 4	222	2.9	5767	3	Sequence 19, Appl
C 5	222	2.9	14446	3	Sequence 3, Appl
C 6	221	2.9	2728	3	Sequence 4, Appl
C 7	175	2.3	532	3	Sequence 7, Appl
C 8	175	2.3	532	3	Sequence 1, Appl
C 9	175	2.3	532	3	Sequence 1, Appl
C 10	175	2.3	532	3	Sequence 1, Appl
C 11	175	2.3	532	3	Sequence 1, Appl
C 12	175	2.3	532	3	Sequence 1, Appl
C 13	175	2.3	532	3	Sequence 1, Appl
C 14	175	2.3	532	3	Sequence 1, Appl
C 15	175	2.3	532	3	Sequence 1, Appl
C 16	175	2.3	7378	3	Sequence 9, Appl
C 17	175	2.3	7378	3	Sequence 9, Appl
C 18	175	2.3	7378	3	Sequence 9, Appl
C 19	175	2.3	7378	3	Sequence 9, Appl
C 20	175	2.3	7378	3	Sequence 9, Appl
C 21	175	2.3	7378	3	Sequence 9, Appl
C 22	175	2.3	7378	3	Sequence 9, Appl
C 23	175	2.3	7378	3	Sequence 9, Appl
C 24	175	2.3	7378	3	Sequence 9, Appl

C 25	98	1.3	12614	3	US-09-577-424-1	Sequence 1, Appl
C 26	97	1.3	332	3	US-09-028-819-11	Sequence 11, Appl
C 27	97	1.3	332	3	US-09-556-163-11	Sequence 11, Appl
C 28	97	1.3	499	3	US-09-028-819-12	Sequence 12, Appl
C 29	97	1.3	499	3	US-09-556-163-12	Sequence 12, Appl
C 30	97	1.3	978	2	US-08-446-486-31	Sequence 31, Appl
C 31	97	1.3	978	2	US-08-463-308-31	Sequence 31, Appl
C 32	97	1.3	979	2	US-08-446-486-30	Sequence 30, Appl
C 33	97	1.3	979	2	US-08-463-308-30	Sequence 30, Appl
C 34	97	1.3	980	9	5254799-30	Patent No. 5254799
C 35	97	1.3	1034	3	US-09-363-970-35	Sequence 35, Appl
C 36	97	1.3	1303	3	US-08-894-440-2	Sequence 2, Appl
C 37	97	1.3	1303	3	US-09-458-093-2	Sequence 2, Appl
C 38	97	1.3	1600	3	US-09-028-819-14	Sequence 14, Appl
C 39	97	1.3	1600	3	US-09-556-163-14	Sequence 14, Appl
C 40	97	1.3	5033	2	US-08-038-768A-1	Sequence 1, Appl
C 41	97	1.3	7811	2	US-08-549-680A-5	Sequence 5, Appl
C 42	96	1.3	831	2	US-08-450-834-5	Sequence 5, Appl
C 43	96	1.3	4544	3	US-09-488-270A-1	Sequence 1, Appl
C 44	96	1.3	4583	3	US-08-810-720-9	Sequence 9, Appl
C 45	93	1.2	439	2	US-08-247-809A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-10-012-070A-46/c
; Sequence 46, Application US/10012070A
; Patent No. 6867293
; GENERAL INFORMATION:
; APPLICANT: Hawkes, Timothy
; APPLICANT: Warner, Simon
; APPLICANT: Andrews, Christopher
; APPLICANT: Bachoo, Satvinder
; APPLICANT: Pickerill, Andrew
; TITLE OF INVENTION: Herbicide Resistant Plants
; FILE REFERENCE: 50490/UST
; CURRENT APPLICATION NUMBER: US/10/012,070A
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/GB00/01573
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 323
; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-10-012-070A-46

Query Match	3.9%	Score 299;	DB 3;	Length 323;
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Db	143	AGTGACAGATAGCTGGGCAATGGAAATCGAGAGGTTTCCCGATATTACCTTTGTTGA	84	
QY	6438	AAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATCTTTGGAGTAGAC	6496	
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; Sequence 4, Application US/09810861B
; Patent No. 6770799
; GENERAL INFORMATION:
; APPLICANT: Mot. Teafir S.
; APPLICANT: Soreq, Hermona
; APPLICANT: Arentzen, Charles J.
; APPLICANT: Mason, Hugh S.
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
; TITLE OF INVENTION: TRANSGENIC PLANTS
; FILE REFERENCE: BTI-45
; CURRENT APPLICATION NUMBER: US/09/810,861B
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,440
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4
; LENGTH: 14446
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11862)..(12157)
; OTHER INFORMATION: Description of Artificial Sequence: plasmid vector
; OTHER INFORMATION: pTM036. Identity of sequence residues 11862-12157 unknown.
US-09-810-861B-4

Query Match 2.9%; Score 222; DB 3; Length 14446;

Best Local Similarity 100.0%; Pred. No. 6.7e-75; Indels 0; Gaps 0;
Matches 222; Conservative 0; Mismatches 0;

QY 6300 TCTTGAACGATAGCCCTTCTTTATCGCAATGATGCAATTTGTAGAAGCCATCTTCCTTT 6359
Db 13991 TCTTGAACGATAGCCCTTCTTTATCGCAATGATGCAATTTGTAGAAGCCATCTTCCTTT 13932
QY 6360 TCTACTGCTCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCC 6419
Db 13931 TCTACTGCTCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCC 13872
QY 6420 GATATTACCTTTGTTGAAAGCTCTCAATAGCCCTCTGCTCTCTGAGACTGTATCTTTG 6479
Db 13871 GATATTACCTTTGTTGAAAGCTCTCAATAGCCCTCTGCTCTCTGAGACTGTATCTTTG 13812
QY 6480 ATATTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTTG 6521
Db 13811 ATATTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTTG 13770

RESULT 6

US-08-836-402B-7/c
; Sequence 7, Application US/08836402B
; Patent No. 6063988
; GENERAL INFORMATION:
; APPLICANT: Rudiger Hain, Regina Fischer
; TITLE OF INVENTION: DNA SEQUENCE AND ITS USE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG KRAMER SCHAEFER & BRISCOE
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Gateway 2000
; OPERATING SYSTEM: DOS
; SOFTWARE: Microsoft Windows 98
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,402B
; FILING DATE: 02-SEP-1997

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 44 40 200.7 (Germany)
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 9840-KGB
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2728 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
US-08-836-402B-7

Query Match 2.9%; Score 221; DB 3; Length 2728;

Best Local Similarity 100.0%; Pred. No. 2.1e-74; Indels 0; Gaps 0;
Matches 221; Conservative 0; Mismatches 0;

QY 6300 TCTTGAACGATAGCCCTTCTTTATCGCAATGATGCAATTTGTAGAAGCCATCTTCCTTT 6359
Db 516 TCTTGAACGATAGCCCTTCTTTATCGCAATGATGCAATTTGTAGAAGCCATCTTCCTTT 457
QY 6360 TCTACTGCTCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCC 6419
Db 456 TCTACTGCTCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCC 397
QY 6420 GATATTACCTTTGTTGAAAGCTCTCAATAGCCCTCTGCTCTCTGAGACTGTATCTTTG 6479
Db 396 GATATTACCTTTGTTGAAAGCTCTCAATAGCCCTCTGCTCTCTGAGACTGTATCTTTG 337
QY 6480 ATATTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTT 6520
Db 336 ATATTCTTGGAGTAGACGAGAGTGTGCTGCTCCACCATGTT 296

RESULT 7

US-09-042-426-1/c
; Sequence 1, Application US/09042426
; Patent No. 6114608
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6114608artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,426
; FILING DATE: March 13, 1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614

TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
US-09-042-426-1

Query Match 2.3%; Score 175; DB 3; Length 532;
Best Local Similarity 99.3%; Pred. No. 7.9e-57;
Matches 275; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGTGGAAGACGTTGGTGGAAACGTCCTTTTCCACGA 6249
DB 289 AGATATCACATCAATCCACTTGTGGAAGACGTTGGTGGAAACGTCCTTTTCCACGA 230
QY 6250 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 6309
DB 229 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 170
QY 6310 TAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCTACTGTCC 6369
DB 169 TAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCTACTGTCC 110
QY 6370 TTTGATGAAGTGCAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 6429
DB 109 TTTGATGAAGTGCAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 50
QY 6430 TTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA 6466
DB 49 TTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA 13

RESULT 9
US-09-330-760-1/c
; Sequence 1, Application US/09330760
; Patent No. 6229075
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6229075artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,760
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:

TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
US-09-042-426-1

Query Match 2.3%; Score 175; DB 3; Length 532;
Best Local Similarity 99.3%; Pred. No. 7.9e-57;
Matches 275; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGTGGAAGACGTTGGTGGAAACGTCCTTTTCCACGA 6249
DB 289 AGATATCACATCAATCCACTTGTGGAAGACGTTGGTGGAAACGTCCTTTTCCACGA 230
QY 6250 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 6309
DB 229 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 170
QY 6310 TAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCTACTGTCC 6369
DB 169 TAGCCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCTACTGTCC 110
QY 6370 TTTGATGAAGTGCAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 6429
DB 109 TTTGATGAAGTGCAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 50
QY 6430 TTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA 6466
DB 49 TTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA 13

RESULT 8
US-09-291-238-1/c
; Sequence 1, Application US/09291238
; Patent No. 622104
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 622104artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/291,238
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
;
US-09-330-760-1

Query Match          2.3%; Score 175; DB 3; Length 532;
Best Local Similarity 99.3%; Pred. No. 7.9e-57;
Matches 275; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTCTTGAAGACGTGGTGGAAACGTCCTTTTCCACGA 6249
Db 289 AGATATCACATCAATCCACTTCTTGAAGACGTGGTGGAAACGTCCTTTTCCACGA 230
QY 6250 TCTTCTCGTGGGTGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCATCTTGAACGA 6309
Db 229 TCTTCTCGTGGGTGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCATCTTGAACGA 170
QY 6310 TAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTCTACTGTCC 6369
Db 169 TAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTCTACTGTCC 110
QY 6370 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 6429
Db 109 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 50
QY 6430 TTTGTGAAAAGTCTCAATAGCCCTCTGCTTCTTGA 6466
Db 49 TTTGTGAAAAGTCTCAATAGCCCTCTGCTTCTTGA 13
```

```
RESULT 10
US-09-328-473-1/c
; Sequence 1, Application US/09328473
; Patent No. 6232533
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 623253artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,473
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
```

```
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
;
US-09-328-473-1

Query Match          2.3%; Score 175; DB 3; Length 532;
Best Local Similarity 99.3%; Pred. No. 7.9e-57;
Matches 275; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTCTTGAAGACGTGGTGGAAACGTCCTTTTCCACGA 6249
Db 289 AGATATCACATCAATCCACTTCTTGAAGACGTGGTGGAAACGTCCTTTTCCACGA 230
QY 6250 TCTTCTCGTGGGTGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCATCTTGAACGA 6309
Db 229 TCTTCTCGTGGGTGGGTCCATCTTTGGGACCACTGTGCGTAGAGGCATCTTGAACGA 170
QY 6310 TAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTCTACTGTCC 6369
Db 169 TAGCCTTTCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTCTACTGTCC 110
QY 6370 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 6429
Db 109 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 50
QY 6430 TTTGTGAAAAGTCTCAATAGCCCTCTGCTTCTTGA 6466
Db 49 TTTGTGAAAAGTCTCAATAGCCCTCTGCTTCTTGA 13
```

```
RESULT 11
US-09-330-737-1/c
; Sequence 1, Application US/09330737
; Patent No. 6232534
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 623253artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,737
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
```

```

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-330-737-1

Query Match      2.3%; Score 175; DB 3; Length 532;
Best Local Similarity 99.3%; Pred. No. 7.9e-57;
Matches 275; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTCTTTGAAGACGTGGTTGGAACGTCCTTTTCCACGA 6249
Db 289 AGATATCACATCAATCCACTTCTTTGAAGACGTGGTTGGAACGTCCTTTTCCACGA 230
QY 6250 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGCGGTAGAGGCATCTTGAACGA 6309
Db 229 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGCGGTAGAGGCATCTTGAACGA 170
QY 6310 TAGCCCTTCTTTATCGCAATGATGCGCATTTGTGAAGCCATCTTCTTTCTACTGTCC 6369
Db 169 TAGCCCTTCTTTATCGCAATGATGCGCATTTGTGAAGCCATCTTCTTTCTACTGTCC 110
QY 6370 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 6429
Db 109 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 50
QY 6430 TTTGTTGAAAAGTCTCAATAGCCCTCTGCTCTCTGA 6466
Db 49 TTTGTTGAAAAGTCTCAATAGCCCTCTGCTCTCTGA 13
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RESULT 12
US-09-329-169-1/c
; Sequence 1, Application US/09329169
; Patent No. 6329575
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/329,169
; FILING DATE: 09-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,426
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
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```

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-329-169-1

Query Match      2.3%; Score 175; DB 3; Length 532;
Best Local Similarity 99.3%; Pred. No. 7.9e-57;
Matches 275; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTCTTTGAAGACGTGGTTGGAACGTCCTTTTCCACGA 6249
Db 289 AGATATCACATCAATCCACTTCTTTGAAGACGTGGTTGGAACGTCCTTTTCCACGA 230
QY 6250 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGCGGTAGAGGCATCTTGAACGA 6309
Db 229 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGCGGTAGAGGCATCTTGAACGA 170
QY 6310 TAGCCCTTCTTTATCGCAATGATGCGCATTTGTGAAGCCATCTTCTTTCTACTGTCC 6369
Db 169 TAGCCCTTCTTTATCGCAATGATGCGCATTTGTGAAGCCATCTTCTTTCTACTGTCC 110
QY 6370 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 6429
Db 109 TTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC 50
QY 6430 TTTGTTGAAAAGTCTCAATAGCCCTCTGCTCTCTGA 6466
Db 49 TTTGTTGAAAAGTCTCAATAGCCCTCTGCTCTCTGA 13
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```

RESULT 13
US-09-330-714A-1/c
; Sequence 1, Application US/09330714A
; Patent No. 6342660
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,714A
; FILING DATE: 11-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,426
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
```

	; TYPE: nucleic acid	
	; STRANDEDNESS: double	
	; TOPOLOGY: linear	
	; MOLECULE TYPE: DNA (genomic)	
	; HYPOTHETICAL: NO	
	; ANTI-SENSE: NO	
	; IMMEDIATE SOURCE:	
	; CLONE: 35S Promoter	
	; SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
	US-09-330-714A-1	
	Query Match 2.3%; Score 175; DB 3; Length 532;	
	Best Local Similarity 99.3%; Pred. No. 7.9e-57;	
	Mismatches 2/5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	6190 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTGGAACGTCCTTTTTCCACGA	6249
DB	289 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTGGAACGTCCTTTTTCCACGA	230
QY	6250 TGTTCCTCGTGGGTGGGGTGCATCTTTGGGACCCTGTCGGTAGAGCATCTTTGAACGA	6309
DB	229 TGTTCCTCGTGGGTGGGGTGCATCTTTGGGACCCTGTCGGTAGAGCATCTTTGAACGA	170
QY	6310 TAGCCTTTCCTTTATCGCAATGATGCCATTGTAGAAGCCATCTCTCTTCTACTGTCC	6369
DB	169 TAGCCTTTCCTTTATCGCAATGATGCCATTGTAGAAGCCATCTCTCTTCTACTGTCC	110
QY	6370 TTTCGATGAAGTGACAGATAGCTGGGCAATGAAATCCGAGGAGGTTTCCCAGATATTACCC	6429
DB	109 TTTCGATGAAGTGACAGATAGCTGGGCAATGAAATCCGAGGAGGTTTCCCAGATATTACCC	50
QY	6430 TTGTGTAAGTCTCAATAGCCCTCTGGTCTTCTGA	6466
DB	49 TTGTGTAAGTCTCAATAGCCCTCTGGTCTTCTGA	13
	RESULT 14	
	US-09-328-826-1/c	
	; Sequence 1, Application US/09328826	
	; Patent No. 6399860	
	; GENERAL INFORMATION:	
	; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi	
	; TITLE OF INVENTION: DNA Construct Containing Bacillus	
	; NUMBER OF SEQUENCES: 11	
	; CORRESPONDENCE ADDRESS:	
	; ADDRESSEE: No. 6399860artis Corporation	
	; STREET: 564 Morris Avenue	
	; CITY: Summit	
	; STATE: New Jersey	
	; COUNTRY: USA	
	; ZIP: 07901	
	; COMPUTER READABLE FORM:	
	; MEDIUM TYPE: Floppy disk	
	; COMPUTER: IBM PC compatible	
	; OPERATING SYSTEM: PC-DOS/MS-DOS	
	; SOFTWARE: Patent In Release #1.0, Version #1.25	
	; CURRENT APPLICATION DATA:	
	; APPLICATION NUMBER: US/09/328,826	
	; Filing DATE: 09-Jun-1999	
	; CLASSIFICATION: <Unknown>	
	; PRIOR APPLICATION DATA:	
	; APPLICATION NUMBER: US/09/042,426	
	; FILING DATE: March 13, 1998	
	; ATTORNEY/AGENT INFORMATION:	
	; NAME: Hoxie, Thomas	
	; REGISTRATION NUMBER: 32,993	
	; REFERENCE/DOCKET NUMBER: 135/1	
	; TELECOMMUNICATION INFORMATION:	
	; TELEPHONE: (919) 541-8614	
	; TELEFAX: (919) 541-8689	
	; INFORMATION FOR SEQ ID NO: 1:	
	; SEQUENCE CHARACTERISTICS:	
	; LENGTH: 532 base pairs	

	; TYPE: nucleic acid	
	; STRANDEDNESS: double	
	; TOPOLOGY: linear	
	; MOLECULE TYPE: DNA (genomic)	
	; HYPOTHETICAL: NO	
	; ANTI-SENSE: NO	
	; IMMEDIATE SOURCE:	
	; CLONE: 35S Promoter	
	; SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
	US-09-328-826-1	
	Query Match 2.3%; Score 175; DB 3; Length 532;	
	Best Local Similarity 99.3%; Pred. No. 7.9e-57;	
	Mismatches 2/5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	6190 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTGGAACGTCCTTTTTCCACGA	6249
DB	289 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTGGAACGTCCTTTTTCCACGA	230
QY	6250 TGTTCCTCGTGGGTGGGGTGCATCTTTGGGACCCTGTCGGTAGAGCATCTTTGAACGA	6309
DB	229 TGTTCCTCGTGGGTGGGGTGCATCTTTGGGACCCTGTCGGTAGAGCATCTTTGAACGA	170
QY	6310 TAGCCTTTCCTTTATCGCAATGATGCCATTGTAGAAGCCATCTCTCTTCTACTGTCC	6369
DB	169 TAGCCTTTCCTTTATCGCAATGATGCCATTGTAGAAGCCATCTCTCTTCTACTGTCC	110
QY	6370 TTTCGATGAAGTGACAGATAGCTGGGCAATGAAATCCGAGGAGGTTTCCCAGATATTACCC	6429
DB	109 TTTCGATGAAGTGACAGATAGCTGGGCAATGAAATCCGAGGAGGTTTCCCAGATATTACCC	50
QY	6430 TTGTGTAAGTCTCAATAGCCCTCTGGTCTTCTGA	6466
DB	49 TTGTGTAAGTCTCAATAGCCCTCTGGTCTTCTGA	13
	RESULT 15	
	US-09-289-170-1/c	
	; Sequence 1, Application US/09289170	
	; Patent No. 6573438	
	; GENERAL INFORMATION:	
	; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi	
	; TITLE OF INVENTION: DNA Construct Containing Bacillus	
	; NUMBER OF SEQUENCES: 11	
	; CORRESPONDENCE ADDRESS:	
	; ADDRESSEE: No. 6573438artis Corporation	
	; STREET: 564 Morris Avenue	
	; CITY: Summit	
	; STATE: New Jersey	
	; COUNTRY: USA	
	; ZIP: 07901	
	; COMPUTER READABLE FORM:	
	; MEDIUM TYPE: Floppy disk	
	; COMPUTER: IBM PC compatible	
	; OPERATING SYSTEM: PC-DOS/MS-DOS	
	; SOFTWARE: Patent In Release #1.0, Version #1.25	
	; CURRENT APPLICATION DATA:	
	; APPLICATION NUMBER: US/09/289,170	
	; Filing DATE: 09-Jun-1999	
	; CLASSIFICATION:	
	; PRIOR APPLICATION DATA:	
	; APPLICATION NUMBER: 09/042,426	
	; FILING DATE: March 13, 1998	
	; ATTORNEY/AGENT INFORMATION:	
	; NAME: Hoxie, Thomas	
	; REGISTRATION NUMBER: 32,993	
	; REFERENCE/DOCKET NUMBER: 135/1	
	; TELECOMMUNICATION INFORMATION:	
	; TELEPHONE: (919) 541-8614	
	; TELEFAX: (919) 541-8689	
	; INFORMATION FOR SEQ ID NO: 1:	
	; SEQUENCE CHARACTERISTICS:	
	; LENGTH: 532 base pairs	

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
US-09-289-170-1
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Query Match		2.3%;	Score 175;	DB 3;	Length 532;
Best Local Similarity		99.3%;	Pred. No. 7.9e-57;		
Matches 275;		Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	6190	AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGTCCTTTTCCACGA	6249		
Db	289	AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGTCCTTTTCCACGA	230		
Qy	6250	TGTTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA	6309		
Db	229	TGTTCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA	170		
Qy	6310	TAGCCTTTCCCTTTATCGCAATGATGSCATTTGTAGAAGCCATCTTTCTACTGTCC	6369		
Db	169	TAGCCTTTCCCTTTATCGCAATGATGSCATTTGTAGAAGCCATCTTTCTACTGTCC	110		
Qy	6370	TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC	6429		
Db	109	TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC	50		
Qy	6430	TTTGTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA	6466		
Db	49	TTTGTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA	13		

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 60.0, Gapext 60.0

Searched: 4172979 seqs, 262114271 residues

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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	98	1.3	11667	US-10-508-263-122	Sequence 122, Appl
C 2	62	0.8	332	US-11-038-981A-5	Sequence 5, Appl
C 3	62	0.8	612	US-11-038-981A-1	Sequence 1, Appl
C 4	62	0.8	835	US-10-391-414-10	Sequence 10, Appl
C 5	62	0.8	1273	US-11-038-981A-18	Sequence 18, Appl
C 6	62	0.8	1273	US-11-038-981A-20	Sequence 20, Appl
C 7	62	0.8	1281	US-11-038-981A-19	Sequence 19, Appl
C 8	62	0.8	1935	US-11-038-981A-25	Sequence 25, Appl
C 9	62	0.8	1935	US-11-038-981A-26	Sequence 26, Appl
C 10	62	0.8	1939	US-11-038-981A-24	Sequence 24, Appl
C 11	62	0.8	1963	US-11-038-981A-27	Sequence 27, Appl
C 12	62	0.8	1963	US-11-038-981A-28	Sequence 28, Appl
C 13	62	0.8	1971	US-11-038-981A-29	Sequence 29, Appl
C 14	62	0.8	3469	US-11-192-801-23	Sequence 23, Appl
C 15	62	0.8	3754	US-11-192-801-15	Sequence 15, Appl
C 16	62	0.8	4149	US-11-192-801-13	Sequence 13, Appl
C 17	59	0.8	125	US-11-038-981A-4	Sequence 4, Appl
C 18	59	0.8	1065	US-11-038-981A-15	Sequence 15, Appl
C 19	59	0.8	1073	US-11-038-981A-17	Sequence 17, Appl
C 20	59	0.8	1073	US-11-038-981A-16	Sequence 16, Appl
C 21	59	0.8	1467	US-11-038-981A-21	Sequence 21, Appl
C 22	59	0.8	1467	US-11-038-981A-22	Sequence 22, Appl
C 23	58	0.8	524	US-11-038-981A-6	Sequence 6, Appl

C 24	58	0.8	1459	7	US-11-038-981A-23	Sequence 23, Appl
C 25	43	0.6	524	6	US-10-986-501-81	Sequence 81, Appl
C 26	43	0.6	687	6	US-10-986-501-103	Sequence 103, Appl
C 27	43	0.6	9808	6	US-10-966-483-43	Sequence 43, Appl
C 28	43	0.6	9808	7	US-11-021-441-33	Sequence 33, Appl
C 29	39	0.5	7142	6	US-10-516-768-22	Sequence 22, Appl
C 30	35	0.5	559	6	US-10-986-501-83	Sequence 83, Appl
C 31	35	0.5	2105	7	US-11-054-389-11	Sequence 11, Appl
C 32	35	0.5	8931	7	US-11-071-651-16	Sequence 16, Appl
C 33	34	0.4	240	7	US-11-038-981A-2	Sequence 2, Appl
C 34	34	0.4	1176	7	US-11-038-981A-11	Sequence 11, Appl
C 35	34	0.4	1184	7	US-11-038-981A-9	Sequence 9, Appl
C 36	34	0.4	1184	7	US-11-038-981A-10	Sequence 10, Appl
C 37	32	0.4	319608	7	US-11-145-703-1	Sequence 1, Appl
C 38	31	0.4	201	6	US-10-995-561-55887	Sequence 55887, A
C 39	31	0.4	201	6	US-10-995-561-56237	Sequence 56237, A
C 40	31	0.4	201	6	US-10-995-561-56446	Sequence 56446, A
C 41	31	0.4	1234	6	US-10-750-185-30828	Sequence 30828, A
C 42	31	0.4	2195	6	US-10-750-185-24652	Sequence 24652, A
C 43	31	0.4	2513	6	US-10-750-185-56860	Sequence 56860, A
C 44	31	0.4	134499	7	US-11-117-187-192	Sequence 192, Appl
C 45	31	0.4	171936	6	US-10-933-025-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-10-508-263-122/c
; Sequence 122, Application US/10508263
; Publication No. US20050260754A1
; GENERAL INFORMATION:
; APPLICANT: BASF Plant Science GmbH
; TITLE OF INVENTION: Constructs and methods for regulating gene expression
; FILE REFERENCE: 53262-20085.00
; CURRENT APPLICATION NUMBER: US/10/508,263
; CURRENT FILING DATE: 2004-09-20
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 122
; LENGTH: 11667
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: suppression
; OTHER INFORMATION: construct 2 p3300.1-Toc159-GFP-RNAi
US-10-508-263-122

Query Match	1.3%	Score 98;	DB 6;	Length 11667;
Best Local Similarity	99.3%	Pred. No. 1.1e-27;		
Matches 148;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	6374	GATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCGATATTACCTTTG	6433	
Db	8757	GATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCGATATTACCTTTG	8698	
QY	6434	TTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATCTTGGAGTA	6493	
Db	8697	TTGAAAAGTCTCAATAGCCCTTGGTCTTCTGAGACTGTATCTTTGATATCTTGGAGTA	8638	
QY	6494	GACGAGAGTGTCGTCTCCACCATGTTGG	6522	
Db	8637	GACGAGAGTCTCGTCTCTCCACCATGTTGG	8609	

RESULT 2

US-11-038-981A-5/c
; Sequence 5, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Pang, Sheng Z

```
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 5
; LENGTH: 332
; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-11-038-981A-5

Query Match          0.8%; Score 62; DB 7; Length 332;
Best Local Similarity 100.0%; Pred. No. 4.5e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCATCATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 6249
Db 122 AGATATCATCATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 63

QY 6250 TG 6251
Db 62 TG 61

RESULT 3
US-11-038-981A-1/c
; Sequence 1, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Plasinski, Stanislaw
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 1
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-11-038-981A-1

Query Match          0.8%; Score 62; DB 7; Length 612;
Best Local Similarity 100.0%; Pred. No. 4.2e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCATCATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 6249
Db 526 AGATATCATCATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 467

QY 6250 TG 6251
Db 466 TG 465

RESULT 4
US-10-391-414-10/c
; Sequence 10, Application US/10391414
; Publication No. US20050278799A1
; GENERAL INFORMATION:
; APPLICANT: SHINOZAKI, Kazuko
; APPLICANT: KATSURA, Koji
; APPLICANT: ITO, Yusuke
; TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
; FILE REFERENCE: 382.1041
; CURRENT APPLICATION NUMBER: US/10/391,414
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; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: JP 2002-377316
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 835
; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-10-391-414-10

Query Match          0.8%; Score 62; DB 6; Length 835;
Best Local Similarity 100.0%; Pred. No. 4.1e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCATCATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 6249
Db 744 AGATATCATCATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 685

QY 6250 TG 6251
Db 684 TG 683

RESULT 5
US-11-038-981A-18/c
; Sequence 18, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Plasinski, Stanislaw
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 18
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-18

Query Match          0.8%; Score 62; DB 7; Length 1273;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCATCATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 6249
Db 134 AGATATCATCATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 75

QY 6250 TG 6251
Db 74 TG 73

RESULT 6
US-11-038-981A-20/c
; Sequence 20, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Plasinski, Stanislaw
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
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; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 20
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-20

Query Match          0.8%; Score 62; DB 7; Length 1273;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 6249
Db 898 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 839

QY 6250 TG 6251
Db 838 TG 837

RESULT 7
US-11-038-981A-19/c
; Sequence 19, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 19
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-19

Query Match          0.8%; Score 62; DB 7; Length 1281;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 6249
Db 524 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 465

QY 6250 TG 6251
Db 464 TG 463

RESULT 8
US-11-038-981A-25/c
; Sequence 25, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
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; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 25
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-25

Query Match          0.8%; Score 62; DB 7; Length 1935;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 6249
Db 644 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 585

QY 6250 TG 6251
Db 584 TG 583

RESULT 9
US-11-038-981A-26
; Sequence 26, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 26
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-26

Query Match          0.8%; Score 62; DB 7; Length 1935;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 6249
Db 727 AGATATCACATCAATCCACTTGTCTTGAAGACGTGGTTGGAACGTCCTCTTTTCCACGA 786

QY 6250 TG 6251
Db 787 TG 788

RESULT 10
US-11-038-981A-24/c
; Sequence 24, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
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; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 24
; LENGTH: 1939
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-24

Query Match 0.8%; Score 62; DB 7; Length 1939;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 6249
Db 333 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 274

QY 6250 TG 6251
Db 273 TG 272

RESULT 11
US-11-038-981A-27/c
; Sequence 27, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Plasinski, Stanislaw
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 27
; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-27

Query Match 0.8%; Score 62; DB 7; Length 1963;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 6249
Db 822 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 763

QY 6250 TG 6251
Db 762 TG 761

RESULT 12
US-11-038-981A-28
; Sequence 28, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Plasinski, Stanislaw
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong

; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 28
; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-28

Query Match 0.8%; Score 62; DB 7; Length 1963;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 6249
Db 905 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 964

QY 6250 TG 6251
Db 965 TG 966

RESULT 13
US-11-038-981A-29/c
; Sequence 29, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Plasinski, Stanislaw
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 29
; LENGTH: 1971
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-29

Query Match 0.8%; Score 62; DB 7; Length 1971;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 6249
Db 1135 AGATATCACATCAATCCACTTGCCTTTGAAGACGTGGTTGGAACGCTCTCTTTTCCACGA 1076

QY 6250 TG 6251
Db 1075 TG 1074

RESULT 14
US-11-192-801-23/c
; Sequence 23, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

; CURRENT APPLICATION NUMBER: US/11/192,801
; PRIOR FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 3469
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; FEATURE:
; NAME/KEY: intron
; LOCATION: (654)..(734)
; OTHER INFORMATION: L-Ta.hcb1
; FEATURE:
; NAME/KEY: intron
; LOCATION: (748)..(1238)
; OTHER INFORMATION: I-Os.Act1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1241)..(3199)
; OTHER INFORMATION: Cry3Bb1 variant 11231mv2
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (3217)..(3450)
; OTHER INFORMATION: T-Ta.hsp17
; OTHER INFORMATION: T-Ta.hsp17
US-11-192-801-23

Query Match 0.8%; Score 62; DB 7; Length 3469;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGTGAGACGTGTTGAGACGTGTTGAGACGTGTTCTTTTCCACGA 6249
|||
Db 553 AGATATCACATCAATCCACTTGTGAGACGTGTTGAGACGTGTTCTTTTCCACGA 494
|||
QY 6250 TG 6251
|||
Db 493 TG 492

RESULT 15

US-11-192-801-15/c
; Sequence 15, Application US/11192801
; Publication No. US20050273862A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 3754
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette

; FEATURE:
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; FEATURE:
; NAME/KEY: intron
; LOCATION: (669)..(1472)
; OTHER INFORMATION: I-Zm.Hsp70
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1490)..(3448)
; OTHER INFORMATION: Cry3Bb1 variant v11231
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (3475)..(3730)
; OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
; OTHER INFORMATION: termination and polyadenylation sequence
US-11-192-801-15

Query Match 0.8%; Score 62; DB 7; Length 3754;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCACATCAATCCACTTGTGAGACGTGTTGAGACGTGTTCTTTTCCACGA 6249
|||
Db 553 AGATATCACATCAATCCACTTGTGAGACGTGTTGAGACGTGTTCTTTTCCACGA 494
|||
QY 6250 TG 6251
|||
Db 493 TG 492

Search completed: December 31, 2005, 20:22:35
Job time : 470 secs

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OM nucleic - nucleic search, using sw model
Run on: December 31, 2005, 05:24:09 ; Search time 17827 Seconds
(without alignments)
19893.761 Million cell updates/sec

Title: US-10-650-249-1
Perfect score: 7580
Sequence: 1 agctctattaattcaagaga.....gcgcacccgggtgagact 7580

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size: 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hc:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gsa1:
10: gb_gsa2:
11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	726	9.6	1466	4	CNS0A60U	BX822604 Arabidops
2	717	9.5	736	10	CW802337	CW802337 WiscDsLox
3	711	9.4	720	10	CW797151	CW797151 WiscDsLox
4	708	9.3	1371	4	CNS0A578	BX822618 Arabidops
5	580	7.7	868	8	DR749973	DR749973 79-L02582
6	580	7.7	972	8	DR750042	DR750042 79-L02144
7	528	7.0	528	10	CNS00PNT	AL084743 Arabidops
8	411	5.4	866	8	DR750041	DR750041 79-L02144
9	403	5.3	486	9	B26529	B26529 P9G12TF IGF
10	382	5.0	433	9	B97814	B97814 F18P18TFB I
11	369	4.9	452	9	AQ011657	AQ011657 F24E16TFB
12	323	4.3	441	7	CK437874	CK437874 GQ0042.BR
13	273	3.6	446	1	AA585745	AA585745 28394 Lam
14	98	1.3	199	9	AQ361597	AQ361597 mgxb0004F
15	98	1.3	492	9	AQ361936	AQ361936 mgxb0005M
16	96	1.3	468	10	CL517384	CL517384 SACS3E03 F
17	96	1.3	690	7	CF854584	CF854584 pSMC001XM
18	96	1.3	839	9	AQ362115	AQ362115 mgxb0003F
19	89	1.2	464	9	BH173054	BH173054 SALK_0015
20	82	1.1	250	8	T22381	T22381 4389 Lambda
21	81	1.1	378	3	BP861585	BP861585 BP861585
22	81	1.1	572	9	CC966736	CC966736 BOIFC82TR

C 23	81	1.1	761	10	CW800801	CW800801 WiscDsLox
C 24	81	1.1	869	10	CW799882	CW799882 WiscDsLox
C 25	81	1.1	1320	4	CNS0A504	BX824803 Arabidops
26	70	0.9	654	10	CG206846	CG206846 TOS0467 T
27	63	0.8	735	10	CZ910009	CZ910009 4018012H0
28	62	0.8	115	9	BH751611	BH751611 SALK_0503
29	62	0.8	158	9	BH748291	BH748291 SALK_0451
30	62	0.8	175	9	BH746616	BH746616 SALK_0452
31	62	0.8	198	10	CG709685	CG709685 1119014D0
32	62	0.8	207	9	BZ587759	BZ587759 3590_1_2
33	62	0.8	210	9	BH638795	BH638795 1008024H0
34	62	0.8	215	9	BH753813	BH753813 SALK_0296
35	62	0.8	219	9	BH747744	BH747744 SALK_0337
36	62	0.8	220	9	BH747438	BH747438 SALK_0174
37	62	0.8	230	9	BH746474	BH746474 SALK_0428
38	62	0.8	242	9	BH638950	BH638950 1008026C0
39	62	0.8	244	9	BH746375	BH746375 SALK_0402
40	62	0.8	248	9	BH254798	BH254798 SALK_0172
41	62	0.8	251	9	BH750171	BH750171 SALK_0371
42	62	0.8	254	9	BH748500	BH748500 SALK_0460
43	62	0.8	256	9	BH748499	BH748499 SALK_0460
44	62	0.8	268	9	BH611919	BH611919 SALK_0318
45	62	0.8	269	9	BH211646	BH211646 SALK_0064

ALIGNMENTS

RESULT 1
CNS0A60U
LOCUS
DEFINITION
CNS0A60U 1466 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTFB52B04 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).
ACCESSION
BX822604.1 GI:42464466
VERSION
HTC; GSLT cDNA
KEYWORDS
Arabidopsis thaliana (thale cress)
SOURCE
Arabidopsis thaliana
ORGANISM
Arabidopsis thaliana
REFERENCE
Castelli V., Aury J.M., Jaillon O., Wincker P., Clepet C.,
Menard M., Cruaud C., Quetier F., Scarpelli C., Schachter V.,
Temple G., Caboche M., Weissenbach J. and Salanoubat M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
2 (bases 1 to 1466)
Direct Submission
Genoscope.
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr]
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_FF/Full
length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
1..1466
/organism="Arabidopsis thaliana"
/mol_type="mRNA"

FEATURES
Source

/db_xref="taxon:3702"	
/clone="GSLTFB52Z504"	
/tissue_type="Flowers and buds"	
/ecotype="Col-0"	
/plasmid="pCMVSPORT_6"	
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/gene="At3g55370"	
ORIGIN	
Query Match	9.6%; Score 726; DB 4; Length 1466;
Best Local Similarity	99.5%; Pred. No. 0;
Matches 1046; Conservative	0; Mismatches 4; Indels 1; Gaps 1;
QY	4340 CTTACTCAACCTCGCATTCTTCGCAAAACATCTCGTCGATTGACACGTCGGCGGTTC 4399
Db	408 CTTACTCAACCTCGCATTCTTCGCAAAACATCTCGTCGATTGACACGTCGGCGGTTC 467
QY	4400 TTGAGGAATGTTCTGTTGGAGAGGCTTTAGGAGGAACAAGAGAAACAAATCCAGATCG 4459
Db	468 TTGAGGAATGTTCTGTTGGAGAGGCTTTAGGAGGAACAAGATTAAGCAATCCAGATCG 527
QY	4460 AAATCTACGGTCGTGTCGATGATACTACTAGTACTTCACTTCACTTCTCTCGC 4519
Db	528 AAATCTACGGTCGTGTCGATGATACTACTAGTACTTCACTTCACTTCTCTCGC 587
QY	4520 CCAAGTTACTCAAAACCTAGCAAGTTTCATAGTACGGTCAAAATCCCGAGTTTAATCC 4579
Db	588 CCAAGTTACTCAAAACCTAGCAAGTTTCATAGTACGGTCAAAATCCCGAGTTTAATCC 647
QY	4580 AACTTGCCCATCTTGCTCTCTCCAAAGCCTTGGAGATTACAAATTCAGACCAACTGGA 4639
Db	648 AACTTGCCCATCTTGCTCTCTCCAAAGCCTTGGAGATTACAAATTCAGACCAACTGGA 707
QY	4640 TTAGATTTTGGTGGAACTCAAAATAGCAACATGATAGTGGTATGAGTTCTAGTGGTGG 4699
Db	708 TTAGATTTTGGTGGAACTCAAAATAGCAACATGATAGTGGTATGAGTTCTAGTGGTGG 767
QY	4700 ATCTGGATGCATGGAGAAATCTCCATCAACAAGCTCAGCAATTCCTTCTTGTATC 4759
Db	768 ATCTGGATGCATGGAGAAATCTCCATCAACAAGTTCAGCAATTCCTTCTTGTATC 827
QY	4760 AACACTACCGGATTGGTGGAACTCTCAAAAGCGTTTATATCCATTACTAGAAGTAAGGA 4819
Db	828 AACACTACCGGATTGGTGGAACTCTCAAAAGCGTTTATATCCATTACTAGAAGTAAGGA 887
QY	4820 GGTGTTAATCAAGGTGAATCTCAACAAGAGTAGTGAATATTCCAATCAGCTAATGTTT 4879
Db	888 GGTGTTAATCAAGGTGAATCTCAACAAGAGTAGTGAATATTCCAATCAGCTAATGTTT 947
QY	4880 AAGCCCTTGATGATTTTCTTCAGCGGGGTTAGCCCAACCAAGAAATGTGAAG 4939
Db	948 AAGCCCTTGATGATTTTCTTCAGCGGGGTTAGCCCAACCAAGAAATGTGAAG 1007
QY	4940 GCGGAGAGAAATGATCAGATCGGGTGGGATGGGATGAGTGAATTAACCTATCAAGA 4999
Db	1008 GCGGAGAGAAATGATCAGATCGGGTGGGATGGGATGAGTGAATTAACCTATCAAGA 1067
QY	5000 AACTTTTGGGTAATATCAACATAAACTCAGGAGGAACGAGGAATACATCATCGGGA 5059
Db	1068 AACTTTTGGGTAATATCAACATAAACTCAGGAGGAACGAGGAATACATCATCGGGA 1127
QY	5060 GGTAAACAGTTCTTGGACCGGTTTCACTCCAACTCAACAGGCCATCTCTCATTTAA 5119
Db	1128 GGTAAACAGTTCTTGGACC-GTTTTCACTCCAACTCAACAGGCCATCTCTCATTTAA 1186
QY	5120 GTACTCAGCACTAGCTATTCTTCATGATCTTTTGTGGTGGGATGATGATGTCCT 5179
Db	1187 GTACTCAGCACTAGCTATTCTTCATGATCTTTTGTGGTGGGATGATGATGTCCT 1246
QY	5180 GTCATCGAGTTATGCTGAGGAGATCAAAACCATGAGCTATATCAAAGGCTAATTTT 5239
Db	1247 GTCATCGAGTTATGCTGAGGAGATCAAAACCATGAGCTATATCAAAGGCTAATTTT 1306
QY	5240 GAGGCTCAAGGAAGGTATCGTTATATAAACTATCTTTTTCATCTTTTAAAGATCTTCA 5299
Db	1307 GAGGCTCAAGGAAGGTATCGTTATATAAACTATCTTTTTCATCTTTTAAAGATCTTCA 1366
QY	5300 AAGTGTGAGTATGTTTATGTTGGCTTCTCGTGATATTTATGTTTATTAAGATTGCT 5359
Db	1367 AAGTGTGAGTATGTTTATGTTGGCTTCTCGTGATATTTATGTTTATTAAGATTGCT 1426
QY	5360 CTTATATATTCGCTATATATAGAGGTGGG 5390
Db	1427 CTTATATATTCGCTATATATAGAGGTGGG 1457
RESULT 2	
LOCUS	CW802337 736 bp DNA linear GSS 23-NOV-2004
DEFINITION	WiscDsLox477-480J24 Arabidopsis thaliana T-DNA insertion flanking sequences Arabidopsis thaliana genomic, genomic survey sequence.
ACCESSION	CW802337
VERSION	CW802337.1 GI:56000165
KEYWORDS	GSS.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	
source	
1..736	
/organism="Arabidopsis thaliana"	
/mol_type="genomic DNA"	
/cultivar="Col-O ecotype"	
/db_xref="taxon:3702"	
/tissue_type="Seeds produced by primary (Basta-resistant) transformants"	
/clone_lib="Arabidopsis thaliana T-DNA insertion flanking sequences"	
/note="Vector: pDS-Lox; Sequence generated in the course of an Arabidopsis T-DNA tagging program. TAIL-PCR was used to generate sequencing templates that represent A.T. genomic DNA flanking the left border of the pDS-Lox T-DNA insert. PCR products were sequenced directly by using the p745 primer 5' AACGTCGCAATGTTATTAAAGTTGTC 3'."	
ORIGIN	
Query Match	9.5%; Score 717; DB 10; Length 736;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 717; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	537 GCCTTTTCGTGAAAATGCGCATGTTCTGTTGGAAATCTAGGAATCTTCTTCTACTAAAG 596
Db	20 GCCTTTTCGTGAAAATGCGCATGTTCTGTTGGAAATCTAGGAATCTTCTTCTACTAAAG 79
QY	597 ATTGGCATCGACGTGTACGATTTCCATTGTATATCTATCTCGATATTTCCACCTTAA 656
Db	80 ATTGGCATCGACGTGTACGATTTCCATTGTATATCTATCTCGATATTTCCACCTTAA 139
QY	657 ATATCTTGAATAATTAGATCAAAATATATATGAGAACATATATTTGATCATTTGTAATA 716
Db	140 ATATCTTGAATAATTAGATCAAAATATATATGAGAACATATATTTGATCATTTGTAATA 199

than 90 percent identity was found. The sequences were also blasted against all TIGR5 introns, and matches longer than 50 bp with 95 percent identity are reported as 'intron found'. The remaining terms for SeqAnalysis describe the outcome of the evaluation of the CDS detected after pairwise alignment with CDS plus pseudogenes from the TIGR5 annotation file. The sequences or contigs for which a full CDS with or without STOP codon was detected, a BLASTp against all TIGR5 protein sequences was performed. Full perfect: 100 percent identity; full good: better than 95 percent identity over more than 95 percent of the sequence; partial good: better than 95 percent identity over less than 95 percent of the sequence; weak similarity: less than 95 percent identity over less than 95 percent of the sequence; no similarity: no hit from BLASTp. Note that the collection contains a few clones for which sequencing was not successful, which could have simple technical reasons. Obviously, information about these clones is missing in the submitted data.

Insert Length: 868 Std Error: 0.00

Seq primer: Seta TCGGTTAACGCTAGCATGGATCTC.

FEATURES

Location/Qualifiers

1..868

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/ecoType="Columbia"

/db_xref="GABI:1452143"

/db_xref="taxon:3702"

/clone="006-G10"

/lab_host="E. coli DH5alpha"

/clone_lib="MP1Z-ADIS-065d"

/notes="Vector: pDONR201; In the context of the EU-funded project REGIA (QLG-CT11999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag1: 5p-AATTCAGCTACACC-3p; RG_tag2: 5p-CATGCAATCCGGGATC-3p). During the lifetime of the project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequenceing at the DNA core facility of the MPI of Plant Breeding Research (ADIS; head: Bernd Weishaar), the plasmids were re-transformed into DH5alpha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GabiPD (<http://gabi.rzpd.de>)."

ORIGIN

Query Match 7.7%; Score 580; DB 8; Length 868;
Best Local Similarity 100.0%; Pred. No. 1.2e-258;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4233 TGGTGAACGTGCTGGATCGCAAAAGTCCATTGCTGAAGCAGCTCTAAATTGGCCTA 4292
DB 73 TGGTGAACGTGCTGGATCGCAAAAGTCCATTGCTGAAGCAGCTCTAAATTGGCCTA 132

QY 4293 GATGTGACTCAACCAATAGTCTGTCTTCAATTAACATAGCTTACTCAACCTC 4352
DB 133 GATGTGACTCAACCAATAGTCTGTCTTCAATTAACATAGCTTACTCAACCTC 192

QY 4353 GCATTTCTGCAAAACATGTGTCGCTATTGGACACGTGGCGGTCTCTTGGAGAAATGTC 4412
DB 193 GCATTTCTGCAAAACATGTGTCGCTATTGGACACGTGGCGGTCTCTTGGAGAAATGTC 252

QY 4413 CTGTTGGAGAGGCTTTAGAGGAACAAGAGAACAAATCCAGATCGAAATCTACGGTGC 4472
DB 253 CTGTTGGAGAGGCTTTAGAGGAACAAGAGAACAAATCCAGATCGAAATCTACGGTGC 312

QY 4473 TGGTCTCGACTGATAATACTACTAGTACTTCACTTCACTTCTTCCGCCAAGTTACTCAA 4532
DB 313 TGGTCTCGACTGATAATACTACTAGTACTTCACTTCTTCCGCCAAGTTACTCAA 372

QY 4533 ACCCTAGCAAGTTTTCATAGCTACGGTCAATCCGGAGTTTAATTCCAACTTCCCATCT 4592
DB 373 ACCCTAGCAAGTTTTCATAGCTACGGTCAATCCGGAGTTTAATTCCAACTTCCCATCT 432

QY 4593 TGCCTCTCTCCAAAGCCTTGGAGATTACAATTCAGCAACACTGGATTAGATTTGGTG 4652
DB 433 TGCCTCTCTCCAAAGCCTTGGAGATTACAATTCAGCAACACTGGATTAGATTTGGTG 492

QY 4653 GAACTCAATATAGCAACATGATAGTGTATAGTTCTAGTGGTGGATCTTGGATGCAT 4712
DB 493 GAACTCAATATAGCAACATGATAGTGTATAGTTCTAGTGGTGGATCTTGGATGCAT 552

QY 4713 GGAGAAATACCTCCATCACAAAGCTCAGCAATTCCTTTCTTGTATCAACACTTACCGGAT 4772
DB 553 GGAGAAATACCTCCATCACAAAGCTCAGCAATTCCTTTCTTGTATCAACACTTACCGGAT 612

QY 4773 TGGTGAATCTTCCAAAGCCTTATATCCATTACTAGAAG 4812
DB 613 TGGTGAATCTTCCAAAGCCTTATATCCATTACTAGAAG 652

RESULT 6
DR750042/c
LOCUS
DEFINITION
979-1021445-065-006-G10-SeqLB MP1Z-ADIS-065d Arabidopsis thaliana
CDNA clone 006-G10, mRNA sequence.

ACCESSION
DR750042
VERSION
DR750042.1
KEYWORDS
GI:71035382
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana

REFERENCE
Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B., Gilman, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R., Coupland, G., Martin, C., Angenent, G. C., Baumeister, H., Mock, H. P., Carbonero, P., Colombo, L., Tonelli, C., Engstroem, P., Droge-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M., Laux, T., Hordsworth, M., Ruberti, I., Ratcliff, F., Smeekens, S., Somsich, I., Weishaar, B. and Traas, J.
REGIA, an EU project on functional genomics of transcription factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002)

JOURNAL
COMMENT
Contact:
Paz-Ares, Costantino, Vittorioso, Davies, Gilman, Giraudat, Parcy, Sablowski, Coupland, Martin, Angenent, Baumeister, Carbonero, Colombo, Tonelli, Engstroem, Droge-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Hordsworth, Ruberti, Smeekens, Somsich, Weishaar, Traas
Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Email: bernd.weishaar@uni-bielefeld.de
AGI: AT3G53370; SeqAnalysis: truncated in 5' at pos 179;
Translation: no full cds detected
Data analysis performed in the frame of REGULATORS (Exploiting inter-species conservation in promoter sequences to identify regulators of reproductive development and physiological performance), a Trilateral Co-Operation in Plant Genomics between Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by G. Coupland (coupland-ad-impz-koeln.mpg.de). Authors: Vincent Thareau (ThP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE, lecharny-ad-ibp.u-psud.fr).
Definition of the terms used to describe the quality of the clone: The about 2250 sequences from the clone collection were sorted according to clones and clustered. If more than one contig was formed, the clone was designated 'contamination'. The contigs and

singletons were blasted against CDS plus pseudogenes from the TIGR5 annotation, and the resulting AGI code is presented if more than 90 percent identity was found. The sequences were also blasted against all TIGR5 introns, and matches longer than 50 bp with 95 percent identity are reported as 'intron found'. The remaining terms for SeqAnalysis describe the outcome of the evaluation of the CDS detected after pairwise alignment with CDS plus pseudogenes from the TIGR5 annotation file. The sequences or contigs for which a full CDS with or without STOP codon was detected, a BLASTp against all TIGR5 protein sequences was performed. Full perfect: 100 percent identity; full good: better than 95 percent identity over more than 95 percent of the sequence; partial good: better than 95 percent identity over less than 95 percent of the sequence; weak similarity: less than 95 percent identity over less than 95 percent of the sequence; no similarity: no hit from BLASTp. Note that the collection contains a few clones for which sequencing was not successful, which could have simple technical reasons. Obviously, information about these clones is missing in the submitted data.

Insert Length: 972 Std Error: 0.00

Seq primer: SELB GTAACATCAGAGATTTTGAGACAC.

FEATURES

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Location/Qualifiers
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/db_xref="GABI:1452133"
/db_xref="taxon:3702"
/clone="006-G10"
/lab_host="E. coli DH5alpha"
/clone_lib="MP1Z-ADIS-065d"
/note="Vector: pDONR201; in the context of the EU-funded project REGIA (QLG-CT11999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag1: 5pr-AATTCACGATCCGCGGATC-3pr; RG_tag2: 5pr-CATGCGAATTCGCGGATC-3pr). During the lifetime of the project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS; head: Bernd Weishaar), the plasmids were re-transformed into DH5alpha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GabiPD (http://gabi.rzpd.de)."
```

ORIGIN

Query Match 7.7%; Score 580; DB 8; Length 972;
Best Local Similarity 100.0%; Pred. No. 1.2e-258;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4233 TGGTGAAGCTGCTCGATCGCAAAAGTCCCATTCGCTGAAGCAGCTCTAAATGGCCCTA 4292
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DB 888 TGGTGAAGCTGCTCGATCGCAAAAGTCCCATTCGCTGAAGCAGCTCTAAATGGCCCTA 829
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QY 4293 GATGTGACCTCAACCAATACTAGTCTCTGTTACTTCAATACTATAGCCTTACTCAACCTC 4352
|||||

DB 828 GATGTGACCTCAACCAATACTAGTCTCTGTTACTTCAATACTATAGCCTTACTCAACCTC 769
|||||

QY 4353 GCCATTCTGCAAAACATGTGTCGCTATTGGACACAGTGGCGGTTCCCTTGAGGAATGTTTC 4412
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DB 768 GCCATTCTGCAAAACATGTGTCGCTATTGGACACAGTGGCGGTTCCCTTGAGGAATGTTTC 709
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QY 4413 CTGTTGGAGGCTTTAGGAGGAACAAGAGCAATCCAGATCGAATCTACGGTCG 4472
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Db 708 CTGTTGGAGGCTTTAGGAGGAACAAGAGCAATCCAGATCGAATCTACGGTCG 649
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QY 4473 TGGTCTCACTGATTAATCTACTAGTACTCATCTACTTCTCGCCCAAGTTACTCAA 4532
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DB 648 TGGTCTCACTGATTAATCTACTAGTACTCATCTACTTCTCGCCCAAGTTACTCAA 589
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QY 4533 ACCCTAGCAAGTTTTCATAGCTACGGTCAAAATCCCGAGGTTTAAATCCCACTTGCCCATCT 4592
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DB 588 ACCCTAGCAAGTTTTCATAGCTACGGTCAAAATCCCGAGGTTTAAATCCCACTTGCCCATCT 529
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QY 4593 TGCCTCTCTCCAAAGCCCTTGAGATTACAATCAAGCAACACTGGATTAGATTTGGTG 4652
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DB 528 TGCCTCTCTCCAAAGCCCTTGAGATTACAATCAAGCAACACTGGATTAGATTTGGTG 469
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QY 4653 GAATCAAAATAGCAACATGATAGTGGTATGATGTTCTAGTGGTGGGATCTTGGATGAT 4712
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DB 468 GAATCAAAATAGCAACATGATAGTGGTATGATGTTCTAGTGGTGGGATCTTGGATGAT 409
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QY 4713 GGAGAAATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACACTACCGGAT 4772
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DB 408 GGAGAAATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACACTACCGGAT 349
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QY 4773 TGGTGCAATCTTCAAAACGCTTTATATCCATTACTAGAAAG 4812
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DB 348 TGGTGCAATCTTCAAAACGCTTTATATCCATTACTAGAAAG 309
|||||

RESULT 7
CNS00PNT
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DEFINITION
Arabidopsis thaliana genome survey sequence T7 end of BAC F9G12 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
AUTHORS
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
FEATURES
Location/Qualifiers
1..528
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_lib="IGF"
/ecotype="Columbia"
/note="end : T7"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.3e-234;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2007 TTTATTTGTTAAAGCATTCTTTCTTAAACAGAGAAATTTACATCATCTTTAGACTGA 2066
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DB 1 TTTATTTGTTAAAGCATTCTTTCTTAAACAGAGAAATTTACATCATCTTTAGACTGA 60
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QY 2067 ACTTTCGGGATAAAAAATCTCGCCATCGCAAGGTAATTTATTTTTCATGACAAAAGCCA 2126
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Db 61 ACTTCGGGATAAAAATCTCGCCATGCAAGGTAATTTATTTTTCATGACAAAAGCCA 120
QY 2127 CAATGCGGTAATTAATACTATAATACTATGCAAAACGAAACTTTACTTGGGTCAACCG 2186
Db 121 CAATGCGGTAATTAATACTATAATACTATGCAAAACGAAACTTTACTTGGGTCAACCG 180
QY 2187 AGGAAACAAAGGTACACTCGATTGTGACAACTCCACCAAGACCAACCCCACTACCAAT 2246
Db 181 AGGAAACAAAGGTACACTCGATTGTGACAACTCCACCAAGACCAACCCCACTACCAAT 240
QY 2247 CACCTTTATTTGTTCTTTATTCACCTCAAAATCTTTTAAATTTTAAATTAATTCAT 2306
Db 241 CACCTTTATTTGTTCTTTATTCACCTCAAAATCTTTTAAATTTTAAATTAATTCAT 300
QY 2307 ATTGCGTTCTCGTGTGTTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 2366
Db 301 ATTGCGTTCTCGTGTGTTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 360
QY 2367 TTTCCTCTCTGATGCGCACTCTCGCTCTTACATCTTTTGGGCAACCTGTTTAAAC 2426
Db 361 TTTCCTCTCTGATGCGCACTCTCGCTCTTACATCTTTTGGGCAACCTGTTTAAAC 420
QY 2427 GTATGCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 2486
Db 421 GTATGCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 480
QY 2487 TGTCGTTCTCTCATAAAAAGAAATTTTAACTTTTAACTTTTAACTTTTAACTTTT 2534
Db 481 TGTCGTTCTCTCATAAAAAGAAATTTTAACTTTTAACTTTTAACTTTTAACTTTT 528

RESULT 8

DR750041

LOCUS

DEFINITION 866 bp mRNA linear EST 19-JUL-2005
79-L021444-065-006-G10-SeLA MP1Z-ADIS-065d Arabidopsis thaliana

ACCESSION

DR750041

VERSION

DR750041.1

KEYWORDS

EST.

SOURCE

Arabidopsis thaliana

ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 866)

Paz-Ares,J., Valencia,A., Costantino,P., Vittorioso,P., Davies,B.,

Gilmarin,P., Giraudat,J., Parcy,E., Reindl,A., Sablowski,R.,

Coupland,G., Martin,C., Angenent,G.C., Baumelein,H., Mock,H.P.,

Carbonero,P., Colombo,L., Tonelli,C., Engstroem,P.,

Droge-Laser,W., Gatz,C., Kavanagh,T., Kushnir,S., Zabeau,M.,

LauX,T., Hordsworth,M., Ruberti,I., Ratcliff,F., Smeekens,S.,

Somsich,I., Weishaar,B. and Traas,J.

REGIA, an EU project on functional genomics of transcription

factors from Arabidopsis thaliana

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Contact:

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Bielefeld University, Institute for Genome Research

Universitaetsstrasse 25, D-33594 Bielefeld, Germany

Email: bernd.weishaar@uni-bielefeld.de

AGI: AT3G55370; SeqAnalysis: truncated in 5' at pos 179;

Translation: no full cds detected

Data analysis performed in the frame of REGULATORS (Exploiting

inter-species conservation in promoter sequences to identify

regulators of reproductive development and physiological

performance), a Trilateral Co-Operation in Plant Genomics between

Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by

G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent

Thareau (thp-orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and

Alain Lechamy (URGV-Evry UMR INRA-CNRS-UEVE,

lechamy-ad-ibp.u-psud.fr).
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percent identity are reported as 'intron found'. The remaining
terms for SeqAnalysis describe the outcome of the evaluation of the
CDS detected after pairwise alignment with CDS plus pseudogenes
from the TIGR5 annotation file. The sequences or contigs for which
a full CDS with or without STOP codon was detected, a BLASTp
against all TIGR5 protein sequences was performed. Full perfect:
100 percent identity; full good: better than 95 percent identity
over more than 95 percent of the sequence; partial good: better
than 95 percent identity over less than 95 percent of the sequence;
weak similarity: less than 95 percent identity over less than 95
percent of the sequence; no similarity: no hit from BLASTp. Note
that the collection contains a few clones for which sequencing was
not successful, which could have simple technical reasons.
Obviously, information about these clones is missing in the
submitted data.

Insert Length: 866 Std Error: 0.00

Seq primer: SeLA TCGGTTAACGCTAGCATGGATCTC.

FEATURES
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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
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/db_xref="GABI:1452132"
/db_xref="taxon:3702"
/clone="006-G10"
/lab_host="E. coli DH5alpha"
/clone_lib="MP1Z-ADIS-065d"
/note="Vector: pDONR201; in the context of the EU-funded
Project REGIA (QLG-CT11999-00876, coordinator Javier
Paz-Ares), a set of transcription factor ORFs was
generated. The ORFs were produced in a decentralized way
in the labs of the participants. Most of the ORFs were
generated by RT-PCR using cDNA from various A. thaliana
tissues as a template. Initially, it was planned to use
yeast recombination to move the ORFs from the cloning
vectors into target constructs. For this reason, a number
of the clones contain 'REGIA tags' (RG_tag1:
5pr-AATTCGAGCTCCACC-3pr; RG_tag2:
5pr-CATGCGAATTCCTCCGGGATC-3pr). During the lifetime of the
project, the GATEWAY system became available and finally
all ORFs were transferred into GATEWAY vectors. At the end
of the REGIA project, the clones were collected as plasmid
DNA. For end-sequencing at the DNA core facility of the
MPI of Plant Breeding Research (ADIS; head: Bernd
Weishaar), the plasmids were re-transformed into
DH5alpha, arrayed into 96-well plates and new plasmid DNA
was prepared. Re-transformation proved to be difficult
because a number of clones displayed poor growth. Data
submission has been handled by Gabipd
(http://gabi.rzpd.de)."

ORIGIN

Query Match 5.4%; Score 411; DB 8; Length 866;
Best Local Similarity 99.5%; Pred. No. 8.6e-180;
Matches 561; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4249 GATCCAAAAGTCCCATTCCTCGCTGAAGCAGCTCTAAATTCCTAGATGACTCAACCA 4308
Db 34 GATCCAAAAGTCCCATTCCTCGCTGAAGCAGCTCTAAATTCCTAGATGACTCAACCA 93
QY 4309 TACTAAGTTCTGTACTTCAATACTATAGCCTTACTCAACCTCGCCATTTCTGCAAAAC 4368
Db 94 TACTAAGTTCTGTACTTCAATACTATAGCCTTACTCAACCTCGCCATTTCTGCAAAAC 153

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QY 4369 ATGTCGTGCTATTGACACAGCGGGCGGTTCTTGTAGGAATGTTCTGTTGGAGGAGGCTT 4428
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QY 4429 TAGGAGGAACAAGAGAAGCAAAATCCAGATCGAAATCTACGGFCGTGGTCTCGACTGATAA 4488
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Db 214 TAGGAGGAACAAGAGAAGCAAAATCCAGATCGAAATCTACGGFCGTGGTCTCGACTGATAA 273
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QY 4489 TACTACTAGTACTTCACTCACTTACTTCTCGCCCAAGTTACTCAAAACCTCAGCAAGTTTCA 4548
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Db 274 TACTACTAGTACTTCACTCACTTACTTCTCGCCCAAGTTACTCAAAATTTTAGCAAGTTTCA 333
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QY 4549 TAGCTACGCTCAAAATCCCGGAGTTTAAATTCCAACTTGGCCATCTTGCCTCTCTCCAAAG 4608
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QY 4609 CTTTGGAGATTACAAATTCGAAGCAACACTGGATTAGATTGTTGGTGAACCTCAAAATGAAGCAA 4668
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QY 4669 CATGATAGTGTATGAGTTCTAGTGGTGGGATCTTGGATGCATGGAGAAATACCTCCATC 4728
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Db 454 CATGATAGTGTATGAGTTCTAGTGGTGGGATCTTGGATGCATGGAGAAATACCTCCATC 513
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QY 4729 ACAACAAGCTCAGCAATCCCTTTCTTGATCAACACTACCGGATTTGGTGCAATCTTCAA 4788
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Db 514 ACAACAAGCTCAGCAATCCCTTTCTTGATCAACACTACCGGATTTGGTGCAATCTTCAA 573
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QY 4789 CGCGTTATATCCATTACTAGAAAG 4812
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Db 574 CGCGTTATATCCATTACTAGAAAG 597
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DEFINITION survey sequence.
ACCESSION B26529
VERSION B26529.1 GI:2512495
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 486)
AUTHORS Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D. and
Venter,J.C.
TITLE Use of a BAC End Sequence Database To Identify Minimal Overlaps for
Arabidopsis Genomic Sequencing
JOURNAL Unpublished (1997)
COMMENT Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
High quality sequence stop: 486.
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Produced by Thomas Altmann"
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Best Local Similarity 100.0%; Pred. No. 4.9e-176;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2031 TCTTAACAGAGGAATTTTACATCATCTTTCAGACTGAACTTTTCGGGATAAAAAATCTCGCC 2090
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Db 8 TCTTAACAGAGGAATTTTACATCATCTTTCAGACTGAACTTTTCGGGATAAAAAATCTCGCC 67
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QY 2091 ATGCAAAAGGTAAATTTATTTTTCATGACAAAGCCACAATGGCGATTAATACTATAA 2150
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Db 68 ATGCAAAAGGTAAATTTATTTTTCATGACAAAGCCACAATGGCGATTAATACTATAA 127
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QY 2151 TACTATGCAAAACGAACTTTTACTTGGGTATACCCGAGGAAAAACAAGGTACACTCGATT 2210
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Db 128 TACTATGCAAAACGAACTTTTACTTGGGTATACCCGAGGAAAAACAAGGTACACTCGATT 187
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QY 2211 GTGCAAACTCCCAACCAAGACCAACCCACTACCAATTCACCTTATTTGTTCTTTATTTCA 2270
|||||
Db 188 GTGCAAACTCCCAACCAAGACCAACCCACTACCAATTCACCTTATTTGTTCTTTATTTCA 247
|||||
QY 2271 CTCAAAACTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 2330
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Db 248 CTCAAAACTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 307
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Db 308 ACCTTTTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 367
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QY 2391 CGCTCTTCACATCTTTTGGGACCACTTGTAACTGATGCA 2433
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RESULT 10
B97814
LOCUS F18P18TFB IGF Arabidopsis thaliana genomic clone F18P18, genomic
DEFINITION survey sequence.
ACCESSION B97814
VERSION B97814.1 GI:2999893
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 433)
AUTHORS Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and
Venter,J.C.
TITLE A BAC End Sequence Database for Identifying Minimal Overlaps in
Arabidopsis Genomic Sequencing. Update 3
JOURNAL Unpublished (1997)
COMMENT Other GSSs: F18P18TR
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
High quality sequence stop: 433.
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FEATURES
source
1. .433
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="F18P18"
```

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/sex="hermaphrodite"
/clone_lib="IGF"
/note="Vector: BelobACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"

ORIGIN
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Best Local Similarity 99.8%; Pred. No. 3.1e-166;
Matches 432; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5459 CTCATTTCTTGGAGACCCATTATGAGACATTTGAGACATCTATGAAACATATATGTAATG 5518
DB 1 CTCATTTCTTGGAGACCCATTATGAGACATTTGAGACATCTATGAAACATATATGTAATG 60

QY 5519 TATATTAACGCTAAAGTCGAATTTTATGACCAAGTAAATAAATATGCGGAATGTA 5578
DB 61 TATATTAACGCTAAAGTCGAATTTTATGACCAAGTAAATAAATATGCGGAATGTA 120

QY 5579 CATGCTAATATCGAGTTTAACTATTTTCCAAATATAACAATATTTCTTTTCGTC 5638
DB 121 CATGCTAATATCGAGTTTAACTATTTTCCAAATATAACAATATTTCTTTTCGTC 180

QY 5639 AACTTATATACCTTATTCGATCTTATTTTCTTTTAAATTCCTTTTCCCTTCC 5698
DB 181 AACTTATATACCTTATTCGATCTTATTTTCTTTTAAATTCCTTTTCCCTTCC 240

QY 5699 AAGACACAAAAAATAACAGAAACGAAAAAAGAGATTTTAAAAATTCATAACCC 5758
DB 241 AAGACACAAAAAATAACAGAAACGAAAAAAGAGATTTTAAAAATTCATAACCC 300

QY 5759 ACGAGAAATATGACCTAAATTCAGACTAATCCCAAAATTCAGAAATTTAATGATTTT 5818
DB 301 ACGAGAAATATGACCTAAATTCAGACTAATCCCAAAATTCAGAAATTTAATGATTTT 360

QY 5819 TCGGATTAATATGTTGTCACATCAATGCGCACTAATTCGAAAGACAATGG 5878
DB 361 TCGGATTAATATGTTGTTCAATCAATGCGCACTAATTCGAAAGACAATGG 420

QY 5879 AATGACTGAAACC 5891
DB 421 AATGACTGAAACC 433

RESULT 11
LOCUS AQ011657
DEFINITION AQ011657 IGF Arabidopsis thaliana genomic clone F24E16, genomic survey sequence.
ACCESSION AQ011657
VERSION AQ011657.1 GI:31666407
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 452)
Rounsley,S.D., Suh,E.J., Wible,C., Golden,K., Shatsman,S., Choi,P., Yu,K., Akinrele,C., Shen,K., Goonasekaram,S., Militscher,J., Adams,M.D. and Venter,J.C.
A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 4
Unpublished (1998)
Other_GSSs: F24E16TR
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends

High quality sequence stop: 452.
Location/Qualifiers
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotType="Columbia"
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/note="Vector: BelobACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"

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Best Local Similarity 99.8%; Pred. No. 3.6e-160;
Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4240 ACGTCTCGGATCGCAAAAGTCCCATTCGCTGAAGCAGCTCTAAATTCGCTAGATGTA 4299
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QY 4480 GACTCATATATCTACTAGTCTTCTACTTCTGCCCCAAGTACTCAAAACCTAG 4539
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QY 4540 CAAATTTTCATAGCTACGGTCAAAATCCCGAGTTTAAATTCCAACTTGGCTCTC 4599
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QY 4600 TCTCCAAAGCCTTGGAGATTACAAATTCAGCACTGATTTAGTATTTGGTGGAACTCA 4659
DB 372 TCTCCAAAGCCTTGGAGATTACAAATTCAGCACTGATTTAGTATTTGGTGGAACTCA 431

RESULT 12
LOCUS CK437874/c
DEFINITION CK437874.1 GI:40768309
ACCESSION CK437874
VERSION CK437874.1
KEYWORDS EST.
SOURCE Picea glauca (white spruce)
ORGANISM Picea glauca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
1 (bases 1 to 441)
Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A., Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J., Siddiqui,A., Holt,R., Marra,M. and Mackay,J.
Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
Contact: John Mackay
Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, CANADA G1K 7P4
Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
```

University of Minnesota, MN id Identifier: MN5176207 Clone ID: GQ0042 P12 Clones available through: John Mackay, Ph. D. Professeur adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
 Plate: 2 row: 12 column: p
 Seq primer: M13 Reverse Primer.

FEATURES

Location/Qualifiers
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 /dev_stage="Non-lignified secondary xylem from trees harvested 2.5 hours, 6 hours and 11 hours after day break"
 /lab_host="E. coli DH10B cells"
 /clone_lib="GQ004: Non-lignified secondary xylem from mature trees"
 /note="Organ: Stem from ground to lower part of live crown, on 33 year old tree; Vector: pBluescript II SK (+) XR; Site: 1: Eco-RI; Site: 2: Xho-I; Tissue was harvested in mid-June, during formation of early wood. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (In vitro) for propagation"

ORIGIN

Query Match 4.3%; Score 323; DB 7; Length 441;
 Best Local Similarity 100.0%; Pred. No. 1e-138;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6190 AGATATCATCATCAATCCACTTCTTGAAGACGTGGTTGGACCGTCTCTTTTCCACGA 6249
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 QY 6250 TGTCTCTGTGGTGGGTGCATCTTGGGACCACTGTCGGTAGAGGATCTTGAACGA 6309
 DB 289 TGTCTCTGTGGTGGGTGCATCTTGGGACCACTGTCGGTAGAGGATCTTGAACGA 230
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 DB 229 TAGCCCTTCTTTATCGCAATGATGCAATTTGTAGAAGCCATCTTCCTTTTCTACTGTC 170
 QY 6370 TTTGATGAAGTCACAGATAGCTGGCAATGGAATCCGAGGAGTTTCCGATATTACCC 6429
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RESULT 13
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 LOCUS 28394 Lambda-PRL2 Arabidopsis thaliana cDNA clone 104F10XP 3', mRNA
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 ACCESSION AA585745
 VERSION AA585745.1 GI:2393157
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

REFERENCE

1 (bases 1 to 446)
 Newman, T., deBruijn, F.J., Green, P., Keestra, K., Kende, H., McIntosh, L., Olligrogge, J., Raikhel, N., Somerville, S., Thomas, M., Retzel, E. and Somerville, C.
 Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 Plant Physiol. 106, 1241-1255 (1994)

TITLE

Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 Plant Physiol. 106, 1241-1255 (1994)

JOURNAL

MSU-DOE Plant Research Laboratory
 Michigan State University

PUBMED

MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI

COMMENT

Contact: Thomas Newman
 Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 22313tcm@bm.cl.msu.edu
 The sequence entry for this EST has been reverse complimented and is being submitted in the sense orientation.

Seq primer: M13 -21 dye primer.

FEATURES

Location/Qualifiers
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 /note="Vector: lambda Zip-Lox; Site 1: Sal; Site 2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA."

ORIGIN

Query Match 3.6%; Score 273; DB 1; Length 446;
 Best Local Similarity 99.7%; Pred. No. 2.2e-115;
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 DB 423 ATGTAATGTATATTAAACGTAATT 446

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AQ361597 199 bp DNA linear GSS 03-FEB-1999
 mgx0004F23f CUGI Rice Blast BAC Library Magnaporthe grisea genomic

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clone mgxb0004F23f, genomic survey sequence.
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SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
REFERENCE 1 (bases 1 to 199)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 96.
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Location/Qualifiers
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/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
ORIGIN
Query Match 1.3%; Score 98; DB 9; Length 199;
Best Local Similarity 99.3%; Pred. No. 1.1e-33;
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 95 TTGAAAAGTCTCAATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTTCTTGAGTA 36
QY 6494 GACGAGAGTGTGCTGCTCCACCATGTTGG 6522
Db 35 GACGAGAGTGTGCTGCTCCACCATGTTGG 7
Search completed: December 31, 2005, 19:00:45
Job time : 17831 secs

clone mgxb0004F23f, genomic survey sequence.
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VERSION AQ361597.1 GI:4211436
KEYWORDS GSS.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
REFERENCE 1 (bases 1 to 199)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 96.
FEATURES
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Location/Qualifiers
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/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
ORIGIN
Query Match 1.3%; Score 98; DB 9; Length 199;
Best Local Similarity 99.3%; Pred. No. 1.1e-33;
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6374 GATGAAGTCACAGATAGCTGGGCAATCGAGAGGTTTCCCGATATTACCTTTTG 6433
Db 155 GATGAAGTCACAGATAGCTGGGCAATCGAGAGGTTTCCCGATATTACCTTTTG 96
QY 6434 TTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTTCTTGAGTA 6493
Db 95 TTGAAAAGTCTCAATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTTCTTGAGTA 36
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Search completed: December 31, 2005, 19:00:45
Job time : 17831 secs

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VERSION AQ361936.1 GI:4211775
KEYWORDS GSS.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
REFERENCE 1 (bases 1 to 492)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 75.
FEATURES
source
Location/Qualifiers
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/organism="Magnaporthe grisea"
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/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
ORIGIN
Query Match 1.3%; Score 98; DB 9; Length 492;
Best Local Similarity 99.3%; Pred. No. 9.9e-34;
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6374 GATGAAGTCACAGATAGCTGGGCAATCGAGAGGTTTCCCGATATTACCTTTTG 6433
Db 155 GATGAAGTCACAGATAGCTGGGCAATCGAGAGGTTTCCCGATATTACCTTTTG 96
QY 6434 TTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTTCTTGAGTA 6493
Db 95 TTGAAAAGTCTCAATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTTCTTGAGTA 36
QY 6494 GACGAGAGTGTGCTGCTCCACCATGTTGG 6522
Db 35 GACGAGAGTGTGCTGCTCCACCATGTTGG 7
Search completed: December 31, 2005, 19:00:45
Job time : 17831 secs

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BEST AVAILABLE COPY

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Db TACATGCTAAGAAAACTCTCTTTTCTGTTCTCTCATAAAAAGAAATTTATTTTAAAC 2520

Qy	2521	TTATTTTAGTCCAAAAATTATTCGTTGCTGATGAAAAATACAATATAGGAAGTGGGATCGG	2581
Db	2521	TTATTTTAGTCCAAAAATTATTCGTTGCTGATGAAAAATACAATATAGGAAGTGGGATCGG	2580
Qy	2581	ATCCGACAAAGAGTGAATTACTACCAACTTAGATTTTCACTCGTCCTTTTGGATGACAAAGT	2640
Db	2581	ATCCGACAAAGAGTGAATTACTACCAACTTAGATTTTCACTCGTCCTTTTGGATGACAAAGT	2640
Qy	2641	AACATACACAATAAACACATATGCATTAATTTTCCATCTTTCAACCAAAATGTTGTAGTGA	2700
Db	2641	AACATACACAATAAACACATATGCATTAATTTTCCATCTTTCAACCAAAATGTTGTAGTGA	2700
Qy	2701	AGTAATTGATCTAATGTTATACGGACATCTATCTATAAATTTTGTGAAAAAATAAAAAA	2760
Db	2701	AGTAATTGATCTAATGTTATACGGACATCTATCTATAAATTTTGTGAAAAAATAAAAAA	2760
Qy	2761	AACATCTATTCATAGTCTCCAAATTAATCTTGCCTTAGTAATTAATGCGGTATATTAGAG	2820
Db	2761	AACATCTATTCATAGTCTCCAAATTAATCTTGCCTTAGTAATTAATGCGGTATATTAGAG	2820
Qy	2821	ATGTTGTTGTTTCTGAAATTTTCATATATGTTCTCTTTTATCTCTGAAATATGATATGCTGA	2880
Db	2821	ATGTTGTTGTTTCTGAAATTTTCATATATGTTCTCTTTTATCTCTGAAATATGATATGCTGA	2880
Qy	2881	ATCATCATAGCATTTTTCAGTGGTTTACAACCTTATCGAATCGACAAAAAGATTGAAACAAAT	2940
Db	2881	ATCATCATAGCATTTTTCAGTGGTTTACAACCTTATCGAATCGACAAAAAGATTGAAACAAAT	2940
Qy	2941	TGGAAAAAATAAAATAGTTTACTATTTTCTTAAGCAGCGTGAAATGAATATCAAGTATAA	3000
Db	2941	TGGAAAAAATAAAATAGTTTACTATTTTCTTAAGCAGCGTGAAATGAATATCAAGTATAA	3000
Qy	3001	TATATGAAACAAATTCCTGACGTGTAATATGTTATACAGTGATACACACCAAGAACGATGA	3060
Db	3001	TATATGAAACAAATTCCTGACGTGTAATATGTTATACAGTGATACACACCAAGAACGATGA	3060
Qy	3061	CGTATATGATTGACTTCGCAAAAAATAAGCAAAACAAATAACCTGTTTCAATCGACACTTAAT	3120
Db	3061	CGTATATGATTGACTTCGCAAAAAATAAGCAAAACAAATAACCTGTTTCAATCGACACTTAAT	3120
Qy	3121	TCCAAAAAGGTTAGTATAAGTAAGAAGGCTTTTATTTATGAAACAAAAAGAAATAAAG	3180
Db	3121	TCCAAAAAGGTTAGTATAAGTAAGAAGGCTTTTATTTATGAAACAAAAAGAAATAAAG	3180
Qy	3181	AGCCTAAGAGAAATGATGAAAAATTGAAAGAGAAAAAAGAGCATTTGTTATAGAAAAGAAAA	3240
Db	3181	AGCCTAAGAGAAATGATGAAAAATTGAAAGAGAAAAAAGAGCATTTGTTATAGAAAAGAAAA	3240
Qy	3241	AAAGAGAGAGTAAGAGAGAAATTAAGAAACACAATAAAATTAACAAAGGAAACTTCATTCT	3300
Db	3241	AAAGAGAGAGTAAGAGAGAAATTAAGAAACACAATAAAATTAACAAAGGAAACTTCATTCT	3300
Qy	3301	TCTCTTTATCCCATTCAGCTCCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAGAT	3360
Db	3301	TCTCTTTATCCCATTCAGCTCCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAGAT	3360
Qy	3361	CAATTCCTTTCTTATGATGATTAATCCACCATATCTGCGACCTCTTAAGAAAAGGA	3420
Db	3361	CAATTCCTTTCTTATGATGATTAATCCACCATATCTGCGACCTCTTAAGAAAAGGA	3420
Qy	3421	TACAAGTAAGAGATTCAAGATGGTTTTCTCATCTCTTCAGTGAATCAGTTCGATCCC	3480
Db	3421	TACAAGTAAGAGATTCAAGATGGTTTTCTCATCTCTTCAGTGAATCAGTTCGATCCC	3480
Qy	3481	AAAAATGGCAGCAGTAAAAATCAGTTTATGATATTTGCTAGATGTTTCTGATTTCGTTCC	3540
Db	3481	AAAAATGGCAGCAGTAAAAATCAGTTTATGATATTTGCTAGATGTTTCTGATTTCGTTCC	3540
Qy	3541	TTTTTCTCTCAGCTCGATCAAGATTTTATGAAAAATTTGATGAGATTTTGTTCGACAAAAAT	3600
Db	3541	TTTTTCTCTCAGCTCGATCAAGATTTTATGAAAAATTTGATGAGATTTTGTTCGACAAAAAT	3600

Qy	3601	TCCTAGCTATTGTGGACGCGCATATATATTACATTATGAAATATTCTTAGTTGATTAACACC	3660
Db	3601	TCCTAGCTATTGTGGACGCGCATATATATTACATTATGAAATATTCTTAGTTGATTAACACC	3660
Qy	3661	TTTTTTTTTCTGTCTTCGAAATATACGAAAAATATATAAAGATGATTTCAATTTTGGTC	3720
Db	3661	TTTTTTTTTCTGTCTTCGAAATATACGAAATATATAAAGATGATTTCAATTTTGGTC	3720
Qy	3721	TTTTTTTCTACTTCAAGACTTTTTTAAAAAATATTCTTAGTTGATAAAAACCTTTTTTCT	3780
Db	3721	TTTTTTTCTACTTCAAGACTTTTTTAAAAAATATTCTTAGTTGATAAAAACCTTTTTTCT	3780
Qy	3781	TGTCCTCTCAAGGGCTTATGTAATATGTTTTTCTTACAGGATTAATTTTCTCTTTGGTT	3840
Db	3781	TGTCCTCTCAAGGGCTTATGTAATATGTTTTTCTTACAGGATTAATTTTCTCTTTGGTT	3840
Qy	3841	AGATTTTTCACACGCGCATGGAAATTACACTTCAAAAATAAAAAAGTTTAAAGTTACTATG	3900
Db	3841	AGATTTTTCACCGCCATGGAAATTACACTTCAAAAATAAAAAAGTTTAAAGTTACTATG	3900
Qy	3901	ACTTTAATCTGAGTTATTTATCCAAATTTCTTTTTCGAGCTTTGTTGAAAACTATAATTA	3960
Db	3901	ACTTTAATCTGAGTTATTTATCCAAATTTCTTTTTCGAGCTTTGTTGAAAACTATAATTA	3960
Qy	3961	ATCTGCAATTCCTTGCACAGTAGTGCAAAATTTTATCTATTTTCTTTTGTCTCCGACAA	4020
Db	3961	ATCTGCAATTCCTTGCACAGTAGTGCAAAATTTTATCTATTTTCTTTTGTCTCCGACAA	4020
Qy	4021	TGTTTTCAAACTCGAATCCTTTTCGTTAAAGTTGTTTTCTGCTTTTATATAAACCCTGAACT	4080
Db	4021	TGTTTTCAAACTCGAATCCTTTTCGTTAAAGTTGTTTTCTGCTTTTATATAAACCCTGAACT	4080
Qy	4081	AAATTAGTACAAATTTATGTTAATATGCAGCAAGGGAACCAACATCAGCTAGAAATGTGCAC	4140
Db	4081	AAATTAGTACAAATTTATGTTAATATGCAGCAAGGGAACCAACATCAGCTAGAAATGTGCAC	4140
Qy	4141	AACTGACCAAGACCCCTAATAATTAATCTTACGCGAGCTCTCATCAACACCGACTTCTCAGGT	4200
Db	4141	AACTGACCAAGACCCCTAATAATTAATCTTACGCGAGCTCTCATCAACACCGACTTCTCAGGT	4200
Qy	4201	TGCAGGTTCCAGTCAAGCTAGAGTGAAATTCAAATGGTGGAAACGTCCTCGGATCCGAAAGT	4260
Db	4201	TGCAGGTTCCAGTCAAGCTAGAGTGAAATTCAAATGGTGGAAACGTCCTCGGATCCGAAAGT	4260
Qy	4261	CCCAATGCCCTGGAAGCAGCTCTAAATTCGCCCTAGATGTGACTCAACCAATACTAAGTTCG	4320
Db	4261	CCCAATGCCCTGGAAGCAGCTCTAAATTCGCCCTAGATGTGACTCAACCAATACTAAGTTCG	4320
Qy	4321	TTACTTCAATAAATATAGCCTTACTCAACCTCCCAATTTCTGCAAAACATGTCTCGCTA	4380
Db	4321	TTACTTCAATAAATATAGCCTTACTCAACCTCCCAATTTCTGCAAAACATGTCTCGCTA	4380
Qy	4381	TTGGACACGTGGCGGTTCCCTTGAGGAATGTTTCTGTTTGAGGAGGCTTTTAGGAGGAACAA	4440
Db	4381	TTGGACACGTGGCGGTTCCCTTGAGGAATGTTTCTGTTTGAGGAGGCTTTTAGGAGGAACAA	4440
Qy	4441	GAGAGCAATCCAGATCGAAATCTACGGTCGTGGTCTCGACTGATAATACTACTAGTAC	4500
Db	4441	GAGAGCAATCCAGATCGAAATCTACGGTCGTGGTCTCGACTGATAATACTACTAGTAC	4500
Qy	4501	TTCAATCACTTACTTCTCGCCCAAGTTACTCAAAACCCCTAGCAAGTTTTCATAGCTACGGTCA	4560
Db	4501	TTCAATCACTTACTTCTCGCCCAAGTTACTCAAAACCCCTAGCAAGTTTTCATAGCTACGGTCA	4560
Qy	4561	AAATCCCGGAGTTTAAATTCCAACTTGCCCAATCTTGGCTCTCTCTCCAAAGCCTTGAGATTA	4620
Db	4561	AAATCCCGGAGTTTAAATTCCAACTTGCCCAATCTTGGCTCTCTCTCCAAAGCCTTGAGATTA	4620
Qy	4621	CAATTCAGCAACACCTGGATTAGATTTTGGTGAACTCAATAAGCAACATGATAGTGG	4680
Db	4621	CAATTCAGCAACACCTGGATTAGATTTTGGTGAACTCAATAAGCAACATGATAGTGG	4680
Qy	4681	TATGATTTCTAGTGGTGGGATCTTGGATGCAATGGAGAAATACCTCCATCAACAAAGCTCA	4740

Db 4681 TATGAGTCTTAGTGTGGGATCTTGGATGCGATGGAGATACCTCCATCAACAAGCTCA 4740
Qy 4741 GCAATTCCTCTTCTTGATCAACACACTACCGGATTTGGTGAATCTTCAAAACGGGTATATCC 4800
Db 4741 GCAATTCCTCTTCTTGATCAACACACTACCGGATTTGGTGAATCTTCAAAACGGGTATATCC 4800
Qy 4801 ATTACTAGAGGTAAAGGAGGTGTTAATCAAGGTGATTTCTCAACAGAGAGTAGTGATTA 4860
Db 4801 ATTACTAGAGGTAAAGGAGGTGTTAATCAAGGTGATTTCTCAACAGAGAGTAGTGATTA 4860
Qy 4861 TTCCCAATCAGCTAAATGTTTAAAGCCCTTGATGATTTTCTCAGCGGGGTTAGCGCCAC 4920
Db 4861 TTCCCAATCAGCTAAATGTTTAAAGCCCTTGATGATTTTCTCAGCGGGGTTAGCGCCAC 4920
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Db 5101 AGGCCATCTCTCATTTCTAAGTACTCAGCACTAGCTATTCTTGATGATTTCTTTGTGGTT 5160
Qy 5161 GGGGTGTAATTTGGTCTTGTCAATGCGAGTTATTTGCTGAGGAAGATCAAAACCATGAGCT 5220
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Qy 5341 TGTTTTATAGAAATTTGGTCTTATATATTTGGCTATATATAGAGGTGGGTGATATGAT 5400
Db 5341 TGTTTTATAGAAATTTGGTCTTATATATTTGGCTATATATAGAGGTGGGTGATATGAT 5400
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Db 5461 CAATTTCTTGGAGACCATATGAGACATTTGAGACATCTATAGAAATATATGATGTA 5520
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Qy 5641 CTTATATCTTATTTCTGATTTCTTATTTTCTTTTAAATCTTTTCTTTTCTTTTCCCAA 5700
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Db 5701 GACACAAAAAATAAATAAGAAACGAAAAAAGAGATTTTAAATAATCAATCAACCCAC 5760
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Db 5761 GAGAAATATGCACTTAATTTCACTAAATTTCCCAAAATTTTCAAGAAATTTATGATTTTGG 5820
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Db 5821 CGATTTAATATGTTGTTTCACAATCATATATGCTTCACTAACTAACTAACTAACTAACTAA 5880
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Qy 5941 ACTATCATCATGATTAAGTAAATGATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 6000
Db 5941 ACTATCATCATGATTAAGTAAATGATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 6000
Qy 6001 ATTTATCTGGATATTAAGATGCGGTTTAAACCTCTTTTGAAGATTTTCTGTTATATCTTTCT 6060
Db 6001 ATTTATCTGGATATTAAGATGCGGTTTAAACCTCTTTTGAAGATTTTCTGTTATATCTTTCT 6060
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Qy 6121 ATCGATCACTTTTATCTTTTGTTCATATGACTACATTTATAGGCTCACACTTTGT 6180
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Qy 6181 TTCCGATCTAGATATCAATCAATCACTTTGCTTTTGAAGAGCTGTTTGAAGCTCTTCTT 6240
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Qy 6241 TTTTCCACCATGTTTCTCGTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGCAT 6300
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Qy 6301 CTTGAAACGATAGCTTTCTTTTATCGCAATGATGCAATTTGTAAGGCCATCTTCTCTTTT 6360
Db 6301 CTTGAAACGATAGCTTTCTTTTATCGCAATGATGCAATTTGTAAGGCCATCTTCTCTTTT 6360
Qy 6361 CTACTGCTCTTTCGATGAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCG 6420
Db 6361 CTACTGCTCTTTCGATGAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCG 6420
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Db 6421 ATATTACCTTTTGTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGA 6480
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Db 6481 TATTCTTGGAGTAGACGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATCACATC 6540
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Qy 6601 GTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCTTTCTT 6660
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7561 GCGCCACCGCGTGAGCT 7580

RESULT 2
US-10-650-249-18
; Sequence 18, Application US/10650249
; Publication No. US20040045055A1
; GENERAL INFORMATION:
; APPLICANT: Neff, Michael M
; TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
; TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
; FILE REFERENCE: WSHU 2064.1
; CURRENT APPLICATION NUMBER: US/10/650,249
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,657
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-18

Query Match 19.8%; Score 1503; DB 7; Length 1746;
Best Local Similarity 99.8%; Pred. No. 0;

Matches 1743; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 4436 AACAGAGAGCAAAATCCAGATCGAAATCTACGGTGGTGGTCTCGACTGATTAATACTACT 4495
DB 1 AACAGAGAGCAAAATCCAGATCGAAATCTACGGTGGTGGTCTCGACTGATTAATACTACT 60
QY 4496 AGTACTTTCATCACTTACTTCTCGCCCAAGTTACTCAAAACCTAGCAAGTTTTCATAGCTAC 4555
DB 61 AGTACTTTCATCACTTACTTCTCGCCCAAGTTACTCAAAACCTAGCAAGTTTTCATAGCTAC 120
QY 4556 GGTCAAAATCCCGGAGTTTAAATTCCAAATCTTGGCCATCTTGGCCCTCTCTCCAAAGCCCTTGA 4615
DB 121 GGTCAAAATCCCGGAGTTTAAATTCCAAATCTTGGCCATCTTGGCCCTCTCTCCAAAGCCCTTGA 180
QY 4616 GATTAACAATTCAGCAACACCTGGATTTAGTTTGGTGGAACTCAAAATAGCAACATGATA 4675
DB 181 GATTAACAATTCAGCAACACCTGGATTTAGTTTGGTGGAACTCAAAATAGCAACATGATA 240
QY 4676 AGTGTATGAGTTCTAGTGGTGGGATCTTGGATGATGGAGAAATACCTCCATCACAACAA 4735
DB 241 AGTGTATGAGTTCTAGTGGTGGGATCTTGGATGATGGAGAAATACCTCCATCACAACAA 300
QY 4736 GCTCAGCAATTCCTCTTCTTGATCAACACTACCGGATTTGGTGAATCTTCAACCGGTTA 4795
DB 301 GCTCAGCAATTCCTCTTCTTGATCAACACTACCGGATTTGGTGAATCTTCAACCGGTTA 360
QY 4796 TATCATTATCTAGAAAGTAAAGGAGGTGTTAATCAAGGTGATTTCAACAGAGAGTAGT 4855
DB 361 TATCATTATCTAGAAAGTAAAGGAGGTGTTAATCAAGGTGATTTCAACAGAGAGTAGT 420
QY 4856 GATTAATTCATCAGCTAATGTTTAAAGCCCTTGATGGATTTTCTTCAGCGGGGTAGC 4915
DB 421 GATTAATTCATCAGCTAATGTTTAAAGCCCTTGATGGATTTTCTTCAGCGGGGTAGC 480
QY 4916 GCCAGCAAAACAAAGAAATGTGAAGCGGGAAGAAATGATCAGGATCGGGGTAGGATGG 4975
DB 481 GCCAGCAAAACAAAGAAATGTGAAGCGGGAAGAAATGATCAGGATCGGGGTAGGATGG 540
QY 4976 GATGAGTGAATTAATCAAGAAATCTTTTGGGTAAATATCAACATAAATCAGGACAG 5035
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QY 5036 AACGAGGATATACATATCGGGGAGTAAAGTCTTGGACCGGTTTCACTCCCAACAC 5095
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QY 5096 TCAACAGGCGCATCTCTCATTTC--TAAAGTACTCAGCACTAGCTATTTTGATGATCTTT 5152
DB 661 TCAACAGGCGCATCTCTCATTTC--TAAAGTACTCAGCACTAGCTATTTTGATGATCTTT 720
QY 5153 TGTGTTGGGTGTACATTTGGTCTTGTTCATGCGAGTTATTTGCTGAGGAAGATCAACAC 5212
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QY 5213 ATGCACTATATCCAAAGCTTAATTTGAGGCTCAAGGAAAGGATGCTTATAAACA 5272
DB 781 ATGCACTATATCCAAAGCTTAATTTGAGGCTCAAGGAAAGGATGCTTATAAACA 840
QY 5273 TCTTTTGTATCTTTTAAAGATCTTCAAGTGTGAGTATGTTTATTTGGTCTTCTGCT 5332
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QY 5333 GATATTTATTTTATTAAGAAATTTGGTCTTATATATTTGGCTATATATAGAGGTGCTGG 5392
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QY 5393 ATATGTATGAATTCAGAGTTGATGTTGAAACCTTTTGTGTTGTTTCTGTTTATTAATCAT 5452
DB 961 ATATGTATGAATTCAGAGTTGATGTTGAAACCTTTTGTGTTGTTTCTGTTTATTAATCAT 1020
QY 5453 CGAATTTCAATTTCTTGGAGACCATATATGAGACATTGAGACATCTATAGAACATATAT 5512
DB 1021 CGAATTTCTCAATTTCTTGGAGACCATATATGAGACATTGAGACATCTATAGAACATATAT 1080

QY	5513	GTAATGTATATTAAGTACTTAAGTCGAATTTTATGACCAAGTAAATTAATATGCGG	5572
Db	1081	GTAATGTATATTAAGTACTTAAGTCGAATTTTATGACCAAGTAAATTAATATGCGG	1140
QY	5573	AATGTACATGCTAATATCGAGTTTAAACATATTTTCCAAATAACAACATATTTCTCTT	5632
Db	1141	AATGTACATGCTAATATCGAGTTTAAACATATTTTCCAAATAACAACATATTTCTCTT	1200
QY	5633	TCGTCCAACTTATATCTTATCTGATTTCTTAATTTTCTCTTTTAAATTCCTTTTCC	5692
Db	1201	TCGTCCAACTTATATCTTATCTGATTTCTTAATTTTCTCTTTTAAATTCCTTTTCC	1260
QY	5693	TTTCCCAAGACACAAAAAATAACAGAAAAGAAAAAGAGATTTTAAAAATTCA	5752
Db	1261	TTTCCCAAGACACAAAAAATAACAGAAAAGAAAAAGAGATTTTAAAAATTCA	1320
QY	5753	TAAACACAGAAATATGACCTTAAATTCAGACTAATCCCAAAATTTTCAGAAAATTATG	5812
Db	1321	TAAACACAGAAATATGACCTTAAATTCAGACTAATCCCAAAATTTTCAGAAAATTATG	1380
QY	5813	TATTTTGGGATTTAATATTTGTTTCAATATCAATATGAGCCCAACTAACTAATTTGAAAAGA	5872
Db	1381	TATTTTGGGATTTAATATTTGTTTCAATATCAATATGAGCCCAACTAACTAATTTGAAAAGA	1440
QY	5873	CAATGGAATGACTGAAACCAATGATTAATCTCAAGTCTCAACCTATGAAGAATCATGTA	5932
Db	1441	CAATGGAATGACTGAAACCAATGATTAATCTCAAGTCTCAACCTATGAAGAATCATGTA	1500
QY	5933	ACCAATAGACTCATGATTTAGTTAATGATGATCTAATATGATTTCTTTGAAACATA	5992
Db	1501	ACCAATAGACTCATGATTTAGTTAATGATGATCTAATATGATTTCTTTGAAACATA	1560
QY	5993	GATATGTCAATTTATCTGGATATAAAGATGGCGTTTTTAACTACTTTTGCAATTTTGTAT	6052
Db	1561	GATATGTCAATTTATCTGGATATAAAGATGGCGTTTTTAACTACTTTTGCAATTTTGTAT	1620
QY	6053	ATCTTTCTTCTAATACATATGATCAATACATCTTTTGTGTTTTTAAAGAAATTTAAACTTTA	6112
Db	1621	ATCTTTCTTCTAATACATATGATCAATACATCTTTTGTGTTTTTAAAGAAATTTAAACTTTA	1680
QY	6113	TTTCAACATCGATCAATTTTACTTTTGTGTTTCCATATGACTACATTTATAGGCTCAC	6172
Db	1681	TTTCAACATCGATCAATTTTACTTTTGTGTTTCCATATGACTACATTTATAGGCTCAC	1740
QY	6173	ACTTTT 6178	
Db	1741	ACTTTT 1746	
RESULT 3			
US-10-033-190-3/c			
; Sequence 3, Application US/10033190			
; Publication No. US20020133848A1			
; GENERAL INFORMATION:			
; APPLICANT: Exelixis Plant Sciences, Inc.			
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF AN ANTHOCYANIN MUTANT (ANT			
; TITLE OF INVENTION: TOMATO			
; FILE REFERENCE: EP01-002C			
; CURRENT APPLICATION NUMBER: US/10/033,190			
; CURRENT FILING DATE: 2001-10-29			
; PRIOR APPLICATION NUMBER: US 60/244,685			
; PRIOR FILING DATE: 2000-10-30			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 3			
; LENGTH: 10078			
; TYPE: DNA			
; ORGANISM: pAG3202			
US-10-033-190-3			
Query Match 18.5%; Score 1402; DB 5; Length 10078;			
Best Local Similarity 100.0%; Pred. No. 0;			

Matches 1402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	6179	GTTCGGATCTAGATATCACATCAATCCATCTGCTTTTGAAGACGCTGTTGGAACGCTTTC	6238
Db	4249	GTTCGGATCTAGATATCACATCAATCCATCTGCTTTTGAAGACGCTGTTGGAACGCTTTC	4190
QY	6239	TTTTTCCACGATGTTCCCTCGTGGGTGGGGTCCATCTTTTGGGACCACCTGTCTCGGTAGAGGC	6298
Db	4189	TTTTTCCACGATGTTCCCTCGTGGGTGGGGTCCATCTTTTGGGACCACCTGTCTCGGTAGAGGC	4130
QY	6299	ATCTTGAACGATAGCTTTTCCCTTTATCGCAATGATGGCAATTTGTAGAGCCATCTTCCCT	6358
Db	4129	ATCTTGAACGATAGCTTTTCCCTTTATCGCAATGATGGCAATTTGTAGAGCCATCTTCCCT	4070
QY	6359	TTCTACTGTCTTTTCGATGAAGTGCACATAGCTGGGCAATGGAATCCGAGGAGGTTTCC	6418
Db	4069	TTCTACTGTCTTTTCGATGAAGTGCACATAGCTGGGCAATGGAATCCGAGGAGGTTTCC	4010
QY	6419	CGATATTACCTTTCTGAAAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTT	6478
Db	4009	CGATATTACCTTTCTGAAAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTT	3950
QY	6479	GATATTTCTGGAGTAGACGAGAGTGTCTGCTTCCACCATGTTGGGATCTAGATATACA	6538
Db	3949	GATATTTCTGGAGTAGACGAGAGTGTCTGCTTCCACCATGTTGGGATCTAGATATACA	3890
QY	6539	TCATATCCACTTGTGTTGAAAGCGTGTGGAAAGTCTTCTTTTCCACGATGTTCTCGT	6598
Db	3889	TCATATCCACTTGTGTTGAAAGCGTGTGGAAAGTCTTCTTTTCCACGATGTTCTCGT	3830
QY	6599	GGGTGGGGTCCATCTTTGGGACCACTGTCTGCTTCCACCATGTTGGGATCTAGATATACA	6658
Db	3829	GGGTGGGGTCCATCTTTGGGACCACTGTCTGCTTCCACCATGTTGGGATCTAGATATACA	3770
QY	6659	TTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTCTACTGTCTTTTCGATGAA	6718
Db	3769	TTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTCTACTGTCTTTTCGATGAA	3710
QY	6719	GTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATATACCTTTGTTGAA	6778
Db	3709	GTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATATACCTTTGTTGAA	3650
QY	6779	AGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTTGTATTTCTTGGAGTAGACGAG	6838
Db	3649	AGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTTGTATTTCTTGGAGTAGACGAG	3590
QY	6839	AGTGTCTGCTCCACCATGTTGGGATCTAGATATCAACATCAATCCATCTGCTTTGAAGA	6898
Db	3589	AGTGTCTGCTCCACCATGTTGGGATCTAGATATCAACATCAATCCATCTGCTTTGAAGA	3530
QY	6899	CGTGTGGAAAGCTCTTTTTCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTGGG	6958
Db	3529	CGTGTGGAAAGCTCTTTTTCACGATGTTCTCTGCTGGGTGGGGTCCATCTTTGGG	3470
QY	6959	ACCACTGTCGGTAGAGGCAATCTTGAACGATAGCTTTCTTTTATCGCAATGATGGCAAT	7018
Db	3469	ACCACTGTCGGTAGAGGCAATCTTGAACGATAGCTTTCTTTTATCGCAATGATGGCAAT	3410
QY	7019	GTAGAAGCCATCTTCTTTTCTACTGTCTCTTTTCTGATGAGTGCACAGATAGCTGGGCAATG	7078
Db	3409	GTAGAAGCCATCTTCTTTTCTACTGTCTCTTTTCTGATGAGTGCACAGATAGCTGGGCAATG	3350
QY	7079	GAAATCCGAGGAGGTTTCCCGATATTTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGCTC	7138
Db	3349	GAAATCCGAGGAGGTTTCCCGATATTTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGCTC	3290
QY	7139	TTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTT	7198
Db	3289	TTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTT	3230
QY	7199	GGGGATCTAGATATCACATCAATCCACTTTGTTGAAAGCGTGGTTGGAACGCTTCTTT	7258
Db	3229	GGGGATCTAGATATCACATCAATCCACTTTGTTGAAAGCGTGGTTGGAACGCTTCTTT	3170

QY 7259 TTCCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATC 7318
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QY 3169 TTCCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATC 3110
QY 7319 TTGAAACGATAGCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTCTTTTC 7378
Db
QY 3109 TTGAAACGATAGCTTTCTTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTCTTTTC 3050
QY 7379 TACTGTCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA 7438
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QY 3049 TACTGTCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA 2990
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QY 2989 TATTACCTTTTGTGAAAAGTCTCAATAGCCCTCTCGGTCTTCTTGAGACTGTATCTTTGAT 2930
QY 7499 ATTCTTGGAGTACACGAGAGTGTCTGCTCCACCATGTTGGGATCCACTAGTTCTAGAG 7558
Db
QY 2929 ATTCTTGGAGTACACGAGAGTGTCTGCTCCACCATGTTGGGATCCACTAGTTCTAGAG 2870
QY 7559 CGGCCGCCACCGCGGTGGAGCT 7580
Db
QY 2869 CGGCCGCCACCGCGGTGGAGCT 2848

RESULT 4

US-09-522-334-1/C
; Sequence 1, Application US/09522334
; Patent No. US20020157130A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Ry
; APPLICANT: Mathews, Helena
; APPLICANT: Liu, Xing Liang
; APPLICANT: Waggoner, Wendy J.
; APPLICANT: Waggoner, Wendy J.
; TITLE OF INVENTION: TRAIT-ASSOCIATED GENE IDENTIFICATION
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 4257-0018.30
; CURRENT APPLICATION NUMBER: US/09/522,334
; CURRENT FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/124,232
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1361
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified enhancer
US-09-522-334-1

Query Match 17.9%; Score 1360; DB 3; Length 1361;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6179 GTTTCGGATCTAGATACATCAATCCACTTGTGGAAGCGTGGTGGAAACGTCCTTC 6238
Db 1360 GTTTCGGATCTAGATACATCAATCCACTTGTGGAAGCGTGGTGGAAACGTCCTTC 1301
QY 6239 TTTTTCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGC 6298
Db 1300 TTTTTCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGC 1241
QY 6299 ATCTTGAACGATAGCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTT 6358
Db 1240 ATCTTGAACGATAGCTTTCTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTT 1181
QY 6359 TTCTACTGTCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCC 6418
Db 1180 TTCTACTGTCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCC 1121
QY 6419 CGATATTACCTTTTGTGAAAAGTCTCAATAGCCCTCTCGTCTCTTGAGACTGTATCTTTT 6478

Db 1120 CGATATTACCTTTTGTGAAAAGTCTCAATAGCCCTCTCGTCTCTTGAGACTGTATCTTT 1061
QY 6479 GATATTCTTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATACACA 6538
Db 1060 GATATTCTTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTGGGGATCTAGATATACACA 1001
QY 6539 TCAATCCACTTCTGTTTGAAGACGTTGGTTCGAAACGTTCTTTTTCACGATGTTCTCGT 6598
Db 1000 TCAATCCACTTCTGTTTGAAGACGTTGGTTCGAAACGTTCTTTTTCACGATGTTCTCGT 941
QY 6599 GGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCCTTTC 6658
Db 940 GGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCCTTTC 881
QY 6659 TTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCTACTGTCTCTTTTCGATGA 6718
Db 880 TTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTCTACTGTCTCTTTTCGATGA 821
QY 6719 GTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTAACCTTTTGTGAAA 6778
Db 820 GTGACAGATAGCTGGGCAATGGAATCCGAGAGGTTTCCCGATATTAACCTTTTGTGAAA 761
QY 6779 AGTCTCAATAGCCCTCTGCTCTCTGAGACTGTATCTTTGTATATCTTCTGAGTAGACGAG 6838
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QY 6839 AGTCTGCTGCTCCACCATGTTGGGATCTAGATATACATCAATCCACTTGTCTTTGAAAGA 6898
Db 700 AGTCTGCTGCTCCACCATGTTGGGATCTAGATATACATCAATCCACTTGTCTTTGAAAGA 641
QY 6899 CTTGTTTGAACGCTCTCTTTTTCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTGGG 6958
Db 640 CTTGTTTGAACGCTCTCTTTTTCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTGGG 581
QY 6959 ACCACTGCTGGTAGAGGCATCTTGAACGATAGCCCTTCTTTTATCGCAATGATGGCATTT 7018
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QY 7079 GAATCCGAGGAGGTTTCCCGATATTAACCTTTTGTGAAAAGTCTCAATAGCCCTCTGCTC 7138
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Db 400 TTCTGAGACTGTATCTTTGATATTTCTTGGAGTAGACGAGTGTCTGCTCCACCATGTT 341
QY 7199 GGGGATCTAGATATCAATCAATCCACTTGTGGAAGCGTGGTGGAAACGTCCTTCTTTT 7258
Db 340 GGGGATCTAGATATCAATCAATCCACTTGTGGAAGCGTGGTGGAAACGTCCTTCTTTT 281
QY 7259 TTCCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCATC 7318
Db 280 TTCCACGATGTTCTCTGTTGGGTGGGGTCCATCTTTTGGGACCACTGTCGGTAGAGGCATC 221
QY 7319 TTGAACGATAGCTTTCTTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTC 7378
Db 220 TTGAACGATAGCTTTCTTTTATCGCAATGATGGCAATTTGTAGAAGCCATCTTCTTTTC 161
QY 7379 TACTGTCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA 7438
Db 160 TACTGTCTTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA 101
QY 7439 TATTACCTTTTGTGAAAAGTCTCAATAGCCCTCTGCTCTTCTGAGACTGTATCTTTGAT 7498
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QY 7499 ATTCTTGGAGTAGACGAGAGTGTCTGCTCCACCATGTTG 7538


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QY 5237 TTTGAGGCTCAAGGAAAGGTATGGTTATATAAACTATCTTTTGTATCTTTTAAAGATCT 5296
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QY 5297 TCAAAGTGTGAGTATGTTTATGCTTGGCTTCTGGTGATATTTATGTTTATTTAGAAATTT 5356
Db 181 TCAAAGTGTGAGTATGTTTATGCTTGGCTTCTGGTGATATTTATGTTTATTTAGAAATTT 240
QY 5357 GGTCTTATATATTTGGCTATATATAGAGGCTGTGGTGATATGATGAAATCAAGAGTTGAT 5416
Db 241 GGTCTTATATATTTGGCTATATATAGAGGCTGTGGTGATATGATGAAATCAAGAGTTGAT 300
QY 5417 GTTGGAAACTTTTGTGCTGCTCAATGAATAATCATCGAATTCCTCAATTTCTTGGAGACC 5476
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QY 5477 CATTTATGAGACATTTGAGACATCTATAGAACATATATGTAATGATATTAACCTACTTAA 5536
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QY 5597 AACTATTTTTCCTCAATATACAACTATTTTCTTTCTGTCGCACTTATATCTTTAT 5656
Db 481 AACTATTTTTCCTCAATATACAACTATTTTCTTTCTGTCGCACTTATATCTTTAT 540
QY 5657 CTGATTTCTTATTTCTTTTAAATTCCTTTTCTTTCCCAAGACACAAAAAATAA 5716
Db 541 CTGATTTCTTATTTCTTTTAAATTCCTTTTCTTTCCCAAGACACAAAAAATAA 600
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QY 5777 AATTGAGACTAATCCCGCAATTTTCAAAATTTATGTAATTTTGGCAATTTATTTGTGT 5836
Db 661 AATTGAGACTAATCCCGCAATTTTCAAAATTTATGTAATTTTGGCAATTTATTTGTGT 720
QY 5837 TCACAAATCAATATGGCCAACTAATTAATGAAAGACAATGGAATGACATGAAACCATGCA 5896
Db 721 TCACAAATCAATATGGCCAACTAATTAATGAAAGACAATGGAATGACATGAAACCATGCA 780
QY 5897 TAATCTCTCAAGTCTCAACCTATGAAGAATCATGTAAACCAATAGACTATCATCATGATTA 5956
Db 781 TAATCTCTCAAGTCTCAACCTATGAAGAATCATGTAAACCAATAGACTATCATCATGATTA 840
QY 5957 GTTAATGCAATGATCTATAATGATATCTTTGAAACATAGATATGTCATTTATCTGGATATA 6016
Db 841 GTTAATGCAATGATCTATAATGATATCTTTGAAACATAGATATGTCATTTATCTGGATATA 900
QY 6017 AGATGGGTTTAACTACTTTCGCAATTTTGTATATCTTTCTTCTTAATACATATGATC 6076
Db 901 AGATGGGTTTAACTACTTTCGCAATTTTGTATATCTTTCTTCTTAATACATATGATC 960
QY 6077 AATACACTTTTGTGTTTAAAGAAATTAATAAATCTTATTTCAACATCGATCAATTTTAA 6136
Db 961 AATACACTTTTGTGTTTAAAGAAATTAATAAATCTTATTTCAACATCGATCAATTTTAA 1020
QY 6137 CTTTGTGTTTCCATTTATGACTACATTTTATAGGCTCACACTTTT 6178
Db 1021 CTTTGTGTTTCCATTTATGACTACATTTTATAGGCTCACACTTTT 1062
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RESULT 7

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US-10-650-249-19
; Sequence 19, Application US/10650249
; Publication No. US20040045055A1
; GENERAL INFORMATION:
; APPLICANT: Neff, Michael M
; TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
; TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
```

```
; FILE REFERENCE: WSHU 2064.1
; CURRENT APPLICATION NUMBER: US/10/650,249
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,657
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1058
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-650-249-19
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Query Match 14.0%; Score 1058; DB 7; Length 1058;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1058; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CAACCAAGAACGATGACGTATATGATTGACTTGCACAAAATAAGCAAAACAAATACCTGTT 60
QY 3105 CAAATCGACACTTAATTCACAAAAGGTTAGTAATAGTAAGAGGCTTTTATTTATGAAA 3164
Db 61 CAAATCGACACTTAATTCACAAAAGGTTAGTAATAGTAAGAGGCTTTTATTTATGAAA 120
QY 3165 ACAAAAGAAATAAGAGGCTTAAGAGATGATGAAATTTGAAAGAGAAAAAGAGCATTTG 3224
Db 121 ACAAAAGAAATAAGAGGCTTAAGAGATGATGAAATTTGAAAGAGAAAAAGAGCATTTG 180
QY 3225 TTATAGAAAGAAAAAGAGAGAGTAAGAGAGTAAGAGACACAATAAATTAACCA 3284
Db 181 TTATAGAAAGAAAAAGAGAGAGTAAGAGAGTAAGAGACACAATAAATTAACCA 240
QY 3285 AGGAAACTTCATTTCTTTTATCCCATTCAGCTCCCTCTCTCTCTCTCTCTCTCTCTCT 3344
Db 241 AGGAAACTTCATTTCTTTTATCCCATTCAGCTCCCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 3345 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3404
Db 301 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
QY 3405 TCTTACCTTAAAGGATCAAGTAAAGATTCACAGATCGTTTCTCATCTCTCTCTCTCTCTCT 3464
Db 361 TCTTACCTTAAAGGATCAAGTAAAGATTCACAGATCGTTTCTCATCTCTCTCTCTCTCT 420
QY 3465 AATCAGTTTCGATTCACAAATTTGGCAGCAGGTAAAAATCAGTTTATGATTTTCTAGAT 3524
Db 421 AATCAGTTTCGATTCACAAATTTGGCAGCAGGTAAAAATCAGTTTATGATTTTCTAGAT 480
QY 3525 GTTCTGATTCGTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3584
Db 481 GTTCTGATTCGTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY 3585 TTTTGTTCGACAAAATTCCTAGCTATTTGGAGCGGCATATATATTTACTTTAGTAATTC 3644
Db 541 TTTTGTTCGACAAAATTCCTAGCTATTTGGAGCGGCATATATATTTACTTTAGTAATTC 600
QY 3645 TTATGTTGATTAACCCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3704
Db 601 TTATGTTGATTAACCCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
QY 3705 GATTTCAATTTTGGTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3764
Db 661 GATTTCAATTTTGGTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
QY 3765 TAAAAACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3824
Db 721 TAAAAACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
QY 3825 AATTTTCTCTTTGTTAGATTTTACACCGCCATGGAATTTATCATTCAAAAAATAAAAA 3884
Db 781 AATTTTCTCTTTGTTAGATTTTACACCGCCATGGAATTTATCATTCAAAAAATAAAAA 840
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QY 3885 GTTTAAAGTTACTATGACCTTTAAATCTGAGTTATTTTATCCATTTTCTTTTTCAGCTTGT 3944
Db 841 GTTTAAAGTTACTATGACCTTTAAATCTGAGTTATTTTATCCATTTTCTTTTTCAGCTTGT 900
QY 3945 TCAAAAACTATAATTAATCTGCAATTCCTGTCAAAGTAGTCAAAATTTTATCTATTTTC 4004
Db 901 TGA AAAAATATAATTAATTAATCTGCAATTCCTGTCAAAGTAGTCAAAATTTTATCTATTTTC 960
QY 4005 TTTTGTCTCCGACCAATGTTTCAAACTCGAATCCTTTTCGTTAAAGTTGTTTCTGCTTTA 4064
Db 961 TTTTGTCTCCGACCAATGTTTCAAACTCGAATCCTTTTCGTTAAAGTTGTTTCTGCTTTA 1020
QY 4065 TTATAAACCTGAAACTAATTAATAGTACAAATTAATGTTAAAT 4102
Db 1021 TTATAAACCTGAAACTAATTAATAGTACAAATTAATGTTAAAT 1058

RESULT 8
US-10-650-249-12
; Sequence 12, Application US/10650249
; Publication No. US20040045055A1
; GENERAL INFORMATION:
; APPLICANT: Neff, Michael M
; TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
; FILE REFERENCE: WSHU 2064.1
; CURRENT APPLICATION NUMBER: US/10/650,249
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,657
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-12

Query Match 11.7%; Score 888; DB 7; Length 888;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4232 ATGGTGGAGCGTCTCGGATCGCAAAAGTCCCATTCGCTGAAGCAGCTCTAAATTCGCCCT 4291
Db 1 ATGGTGGAGCGTCTCGGATCGCAAAAGTCCCATTCGCTGAAGCAGCTCTAAATTCGCCCT 60
QY 4292 AGATGTGACTCAACCAATCTAAGTTCGTGTTACTTCAATAACTATAGCCTTACTCAACCT 4351
Db 61 AGATGTGACTCAACCAATCTAAGTTCGTGTTACTTCAATAACTATAGCCTTACTCAACCT 120
QY 4352 CGCCATTTCTGCAAAACATGTCGCTATTTGACACGCTGGCGGTTCTTTGAGGAATGTT 4411
Db 121 CGCCATTTCTGCAAAACATGTCGCTATTTGACACGCTGGCGGTTCTTTGAGGAATGTT 180
QY 4412 CTGTGTTGGAGGCGCTTTAGGAGGAAACAGAGAAACCAATCCAGATCGAAATCTACGGTC 4471
Db 181 CTGTGTTGGAGGCGCTTTAGGAGGAAACAGAGAAACCAATCCAGATCGAAATCTACGGTC 240
QY 4472 GTGGTCTCGACTGATTAATCTAGTACTTCAATCTACTTCTCGCCCAAGTTACTCA 4531
Db 241 GTGGTCTCGACTGATTAATCTAGTACTTCAATCTACTTCTCGCCCAAGTTACTCA 300
QY 4532 AACCCCTAGCAAGTTTTCATAGCTACGGTCAAAATCCCGAGGTTTAATTTCAACTTTGCCCATC 4591
Db 301 AACCCCTAGCAAGTTTTCATAGCTACGGTCAAAATCCCGAGGTTTAATTTCAACTTTGCCCATC 360
QY 4592 TTGCCTCTCTCAAGCCCTTGAGATTACAATTCAGCAACACTGGATTAGATTTTGGT 4651
Db 361 TTGCCTCTCTCAAGCCCTTGAGATTACAATTCAGCAACACTGGATTAGATTTTGGT 420
QY 4652 GGAACCTCAAAATAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGATCTTTGGATGCA 4711
Db 421 GGAACCTCAAAATAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGATCTTTGGATGCA 480
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QY 4712 TGGGAATACCTCCATCACAACAAGCTCAGCAATTTCCCTTTCTTCTGATCAACAACACTACCGGA 4771
Db 481 TGGGAATACCTCCATCACAACAAGCTCAGCAATTTCCCTTTCTTCTGATCAACAACACTACCGGA 540
QY 4772 TTGGTGCATCTTCAACGCGGTTATATCCATTTACTAGAAAGTAAAGGAGGTGTTAATCAA 4831
Db 541 TTGGTGCATCTTCAACGCGGTTATATCCATTTACTAGAAAGTAAAGGAGGTGTTAATCAA 600
QY 4832 GGTGATTTCTCAACAGAGTAGTATGATTTATTCATAGCTAATGTTTAAAGCCCTTGATG 4891
Db 601 GGTGATTTCTCAACAGAGTAGTATGATTTATTCATAGCTAATGTTTAAAGCCCTTGATG 660
QY 4892 GATTTTCTTTCAGGCGGGTTAGCGCCACGCAAAACAGAAATGTGAAGCGCGGAAGAGAT 4951
Db 661 GATTTTCTTTCAGGCGGGTTAGCGCCACGCAAAACAGAAATGTGAAGCGCGGAAGAGAT 720
QY 4952 GATCAGGATCGGGGTAGGGATGGGGATGGAGTGAATAACTTATCAAGAAACTTTTGGGT 5011
Db 721 GATCAGGATCGGGGTAGGGATGGGGATGGAGTGAATAACTTATCAAGAAACTTTTGGGT 780
QY 5012 AATATCAACATAACTCAGGCGAGGAACGAGGAATACACATCATGGGAGGTAAACAGTTCT 5071
Db 781 AATATCAACATAACTCAGGCGAGGAACGAGGAATACACATCATGGGAGGTAAACAGTTCT 840
QY 5072 TGGACGGGTTTCACTCCAAACAACTCAACAGGCCACTCTCTCATTTCTAA 5119
Db 841 TGGACGGGTTTCACTCCAAACAACTCAACAGGCCACTCTCTCATTTCTAA 888

RESULT 9
US-10-650-249-15
; Sequence 15, Application US/10650249
; Publication No. US20040045055A1
; GENERAL INFORMATION:
; APPLICANT: Neff, Michael M
; TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
; FILE REFERENCE: WSHU 2064.1
; CURRENT APPLICATION NUMBER: US/10/650,249
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,657
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-15

Query Match 9.0%; Score 684; DB 7; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.3e-298;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4436 AACAGAGAGCAATCCAGATCGAAATCTAGCGTCGTCTCGACTGATATACTACT 4495
Db 1 AACAGAGAGCAATCCAGATCGAAATCTAGCGTCGTCTCGACTGATATACTACT 60
QY 4496 AGTACTTCTACTTACTTCTCGCCCAAGTTACTCAAAACCTAGCAAGTTTTCATAGCTAC 4555
Db 61 AGTACTTCTACTTACTTCTCGCCCAAGTTACTCAAAACCTAGCAAGTTTTCATAGCTAC 120
QY 4556 GGTCAAAATCCCGAGGTTTAATTTCCAACTTGCCCATCTTGCTCTCTCCAAAGCCCTTGA 4615
Db 121 GGTCAAAATCCCGAGGTTTAATTTCCAACTTGCCCATCTTGCTCTCTCCAAAGCCCTTGA 180
QY 4616 GATTACAATTCAGCAACACTGGATTAGATTTTGGTGGAACTCAAATAAGCAACATGATA 4675
Db 181 GATTACAATTCAGCAACACTGGATTAGATTTTGGTGGAACTCAAATAAGCAACATGATA 240
QY 4676 AGTGGTATGAGTTCTAGTGGTGGATCTTTGGATGCAATGAGAACTCTCATCAACAA 4735
Db 4676 AGTGGTATGAGTTCTAGTGGTGGATCTTTGGATGCAATGAGAACTCTCATCAACAA 4735
```

Db 241 AGTGGTATGAGTTCTAGTGGTGGATCTTGGATGTCATGGAGTACCTCCATCACAA 300
QY 4736 GCTCAGCAATTCCTTTCTTGATCAACATACCGGATTTGGTGAATCTTCAACCGGTTA 4795
Db 301 GCTCAGCAATTCCTTTCTTGATCAACATACCGGATTTGGTGAATCTTCAACCGGTTA 360
QY 4796 TATCCATTACTAGAAGTGAAGGAGGTGTTAAATCAAGGTGATTTCTCAACAGAGAGTAGT 4855
Db 361 TATCCATTACTAGAAGTGAAGGAGGTGTTAAATCAAGGTGATTTCTCAACAGAGAGTAGT 420
QY 4856 GATTATTTCCAAATCAGCTAATGTTTAAAGCCCTTGATGGATTTTCTCAGCGGGGTAGC 4915
Db 421 GATTATTTCCAAATCAGCTAATGTTTAAAGCCCTTGATGGATTTTCTCAGCGGGGTAGC 480
QY 4916 GCCACGAAACAAAGAAATGTGAAGCGGAGAGAAATGATCAGGATCGGGGTAGGATGGG 4975
Db 481 GCCACGAAACAAAGAAATGTGAAGCGGAGAGAAATGATCAGGATCGGGGTAGGATGGG 540
QY 4976 GATGGAGTGAATTAATCAAGAACTTTTGGGTAATATCAACATAAATCAACTCAGGCAGG 5035
Db 541 GATGGAGTGAATTAATCAAGAACTTTTGGGTAATATCAACATAAATCAACTCAGGCAGG 600
QY 5036 AACGAGGAATACATCATGCGGAGGTAAACAGTTCTTGGACCGGTTTCACTCCAAACAAC 5095
Db 601 AACGAGGAATACATCATGCGGAGGTAAACAGTTCTTGGACCGGTTTCACTCCAAACAAC 660
QY 5096 TCAACAGGCCATCTCTCATTTCTAA 5119
Db 661 TCAACAGGCCATCTCTCATTTCTAA 684

RESULT 10
US-10-487-901-7187
; Sequence 7187, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7187
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-7187

Query Match 7.7%; Score 581; DB 9; Length 645;
Best Local Similarity 100.0%; Pred. No. 5.7e-252;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4232 ATGGTGAAGCTGCTCGGATCGGAAAGTCCATTCGCTGAAGCAGCTCTAAATGCCCT 4291
Db 6 ATGGTGAAGCTGCTCGGATCGGAAAGTCCATTCGCTGAAGCAGCTCTAAATGCCCT 65
QY 4292 AGATGTGACTCAACCAATACTAAGTTCTGTACTTCAATAACTATAGCCTTACTCAACT 4351
Db 66 AGATGTGACTCAACCAATACTAAGTTCTGTACTTCAATAACTATAGCCTTACTCAACT 125

QY 4352 CGCCATTTCTGCARACATGTCGTGCTATTGACACGCTGGCGGTTCTTGAGGAATGTT 4411
Db 126 CGCCATTTCTGCARACATGTCGTGCTATTGACACGCTGGCGGTTCTTGAGGAATGTT 185
QY 4412 CTGTTGGAGGAGGCTTTAGGAGGAAACAAGAGCAAAATCCAGATCGAAATCTACGGTC 4471
Db 186 CTGTTGGAGGAGGCTTTAGGAGGAAACAAGAGCAAAATCCAGATCGAAATCTACGGTC 245
QY 4472 GTGGTCTCGACTGATAAATACTACTAGTACTTCAATCACTTCTCTGCCCAAGTTACTCA 4531
Db 246 GTGGTCTCGACTGATAAATACTACTAGTACTTCAATCACTTCTCTGCCCAAGTTACTCA 305
QY 4532 AACCTTAGCAAGTTTCATAGCTACCGTCAAAATCCCGGAGTTTAAATCCAACTTGGCCATC 4591
Db 306 AACCTTAGCAAGTTTCATAGCTACCGTCAAAATCCCGGAGTTTAAATCCAACTTGGCCATC 365
QY 4592 TTGGCTCTCTCAAGCCCTTGAGATTACAATTTCAAGCAACACTGGATTTAGATTGGT 4651
Db 366 TTGGCTCTCTCAAGCCCTTGAGATTACAATTTCAAGCAACACTGGATTTAGATTGGT 425
QY 4652 GGAATCTCAAAATAGCAACATGATAGTGTGTATGAGTTCTAGTGGTGGGATCTTTGGATGCA 4711
Db 426 GGAATCTCAAAATAGCAACATGATAGTGTGTATGAGTTCTAGTGGTGGGATCTTTGGATGCA 485
QY 4712 TGGAGATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACACTACCGGA 4771
Db 486 TGGAGATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACACTACCGGA 545
QY 4772 TTGGTGCATCTTCAAAACGCTTATATCCATTACTAGAAGG 4812
Db 546 TTGGTGCATCTTCAAAACGCTTATATCCATTACTAGAAGG 586

RESULT 11
US-10-225-066A-409
; Sequence 409, Application US/10225066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CRESLMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI0036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 409
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-409

Query Match 7.7%: Score 581; DB 6; Length 795;
Best Local Similarity 100.0%; Pred. No. 5.8e-252; Indels 0; Gaps 0;
Matches 581; Conservative 0; Mismatches 0;

QY 4232 ATGGTGGAAACGTCGCGATCGAAAGTCCCATTTGCCCTGAAGCAGCTCTAAATTTGCCCT 4291
DB 1 ATGGTGGAAACGTCGCGATCGAAAGTCCCATTTGCCCTGAAGCAGCTCTAAATTTGCCCT 60

QY 4292 AGATGTGACTCAACCAACTACTAAGTTCTGTTACTCAATACTATAGCCTTACTCAACT 4351
DB 61 AGATGTGACTCAACCAACTACTAAGTTCTGTTACTCAATACTATAGCCTTACTCAACT 120

QY 4352 CGCCATTTCTGCAAAACATGTCGCTATTCGACGTCGGCGTTCTTTGAGGAATGTT 4411
DB 121 CGCCATTTCTGCAAAACATGTCGCTATTCGACGTCGGCGTTCTTTGAGGAATGTT 180

QY 4412 CTGTGTTGAGGAGGCTTTAGGAGGAAACAGAGAAATCCAGATCGAAATCTACGGTC 4471
DB 181 CTGTGTTGAGGAGGCTTTAGGAGGAAACAGAGAAATCCAGATCGAAATCTACGGTC 240

QY 4472 GTGGTCTCGACTGATAACTACTAGTACTTCACTTCACTTCTCGCCCAAGTTACTCA 4531
DB 241 GTGGTCTCGACTGATAACTACTAGTACTTCACTTCTCGCCCAAGTTACTCA 300

QY 4532 AACCCCTAGCAAGTTTCATAGCTACGGTCAAAATCCCGGAGTTAAATTCCAACTTGGCCATC 4591
DB 301 AACCCCTAGCAAGTTTCATAGCTACGGTCAAAATCCCGGAGTTAAATTCCAACTTGGCCATC 360

QY 4592 TTGGCTTCCTCTCAAAAGCCTTCGAGATTACAATTCGAAGCAACACTGGATTAGATTGTT 4651
DB 361 TTGGCTTCCTCTCAAAAGCCTTCGAGATTACAATTCGAAGCAACACTGGATTAGATTGTT 420

QY 4652 GGAACCTCAATTAAGCAACATGATAAGTGTATAGTTCCTGAGGATGCTTTGAGATGCA 4711
DB 421 GGAACCTCAATTAAGCAACATGATAAGTGTATAGTTCCTGAGGATGCTTTGAGATGCA 480

QY 4712 TGGAGAAATACCTCCATCAACAAAGCTCAGCAATTCCTTTTCTTGATCAACACTACCGGA 4771
DB 481 TGGAGAAATACCTCCATCAACAAAGCTCAGCAATTCCTTTTCTTGATCAACACTACCGGA 540

QY 4772 TTGGTGCAATCTTCAACCGGTTATATCCATTACTAGAAGG 4812
DB 541 TTGGTGCAATCTTCAACCGGTTATATCCATTACTAGAAGG 581

RESULT 12
US-10-374-780A-2767
; Sequence 2767, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374, 780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2767
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1906
US-10-374-780A-2767

Query Match 7.7%: Score 581; DB 7; Length 795;
Best Local Similarity 100.0%; Pred. No. 5.8e-252;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4232 ATGGTGGAAACGTCGCGATCGAAAGTCCCATTTGCCCTGAAGCAGCTCTAAATTTGCCCT 4291
DB 1 ATGGTGGAAACGTCGCGATCGAAAGTCCCATTTGCCCTGAAGCAGCTCTAAATTTGCCCT 60

QY 4292 AGATGTGACTCAACCAACTACTAAGTTCTGTTACTTCAATACTATAGCCTTACTCAACT 4351
DB 61 AGATGTGACTCAACCAACTACTAAGTTCTGTTACTTCAATACTATAGCCTTACTCAACT 120

QY 4352 CGCCATTTCTGCAAAACATGTCGCTATTCGACGTCGGCGTTCTTTGAGGAATGTT 4411
DB 121 CGCCATTTCTGCAAAACATGTCGCTATTCGACGTCGGCGTTCTTTGAGGAATGTT 180

QY 4412 CTGTGTTGAGGAGGCTTTAGGAGGAAACAGAGAAATCCAGATCGAAATCTACGGTC 4471
DB 181 CTGTGTTGAGGAGGCTTTAGGAGGAAACAGAGAAATCCAGATCGAAATCTACGGTC 240

QY 4472 GTGGTCTCGACTGATAACTACTAGTACTTCACTTCACTTCTCGCCCAAGTTACTCA 4531
DB 241 GTGGTCTCGACTGATAACTACTAGTACTTCACTTCACTTCTCGCCCAAGTTACTCA 300

QY 4532 AACCCCTAGCAAGTTTCATAGCTACGGTCAAAATCCCGGAGTTAAATTCCAACTTGGCCATC 4591
DB 301 AACCCCTAGCAAGTTTCATAGCTACGGTCAAAATCCCGGAGTTAAATTCCAACTTGGCCATC 360

QY 4592 TTGGCTTCCTCTCAAAAGCCTTCGAGATTACAATTCGAAGCAACACTGGATTAGATTGTT 4651
DB 361 TTGGCTTCCTCTCAAAAGCCTTCGAGATTACAATTCGAAGCAACACTGGATTAGATTGTT 420

QY 4652 GGAACCTCAATTAAGCAACATGATAAGTGTATAGTTCCTGAGGATGCTTTGAGATGCA 4711
DB 421 GGAACCTCAATTAAGCAACATGATAAGTGTATAGTTCCTGAGGATGCTTTGAGATGCA 480

QY 4712 TGGAGAAATACCTCCATCAACAAAGCTCAGCAATTCCTTTTCTTGATCAACACTACCGGA 4771
DB 481 TGGAGAAATACCTCCATCAACAAAGCTCAGCAATTCCTTTTCTTGATCAACACTACCGGA 540

QY 4772 TTGGTGCAATCTTCAACCGGTTATATCCATTACTAGAAGG 4812
DB 541 TTGGTGCAATCTTCAACCGGTTATATCCATTACTAGAAGG 581

RESULT 13
US-10-225-066A-409
; Sequence 409, Application US/10225066A
; Publication No. US20050160493A9

```

; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-liang
; APPLICANT: BROWN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MB10036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 409
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-225-066A-409

Query Match          7.7%; Score 581; DB 9; Length 795;
Best Local Similarity 100.0%; Pred. No. 5.8e-252;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4232 ATGGTGAACGTCGCGATCGCAAAAGTCCCATTCGCTGAAGCAGCTCTAAATTGCCCT 4291
DB 1 ATGGTGAACGTCGCGATCGCAAAAGTCCCATTCGCTGAAGCAGCTCTAAATTGCCCT 60

QY 4292 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATTAATCTAGCCCTTACTCAACT 4351
DB 61 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATTAATCTAGCCCTTACTCAACT 120

QY 4352 CGCCATTTCTGCAAAACATGTCGCTATTGGACACGTCGGCGTTCTTGGAGGAATGTT 4411
DB 121 CGCCATTTCTGCAAAACATGTCGCTATTGGACACGTCGGCGTTCTTGGAGGAATGTT 180

QY 4412 CCGTGTGGAGGAGCTTTAGGAGGACAGAGACCAATCCAGATCGAAATCTACGGTC 4471
DB 181 CCGTGTGGAGGAGCTTTAGGAGGACAGAGACCAATCCAGATCGAAATCTACGGTC 240

QY 4472 GTGGTCTCCAGCTGATAACTACTAGTACTTCACTCACTTCTTCGCCCAAGTTACTCA 4531
DB 241 GTGGTCTCCAGCTGATAACTACTAGTACTTCACTCACTTCTTCGCCCAAGTTACTCA 300

QY 4532 AACCCCTAGCAAGTTTCATAGCTACGGTCAAAATCCCGAGTTAAATTCGAATTCGCCCATC 4591
DB 301 AACCCCTAGCAAGTTTCATAGCTACGGTCAAAATCCCGAGTTAAATTCGAATTCGCCCATC 360

QY 4592 TTGGCTCCCTCCAAAGCCCTCGAGATTACAAATTCAGCAACACCTGGATTAGATTTCGT 4651
DB 361 TTGGCTCCCTCCAAAGCCCTCGAGATTACAAATTCAGCAACACCTGGATTAGATTTCGT 420

QY 4652 GGAACTCAAAATAGCAACATGATAGTGTATGAGTTCTAGTGGTGGATCTTTGGATGCA 4711
DB 421 GGAACTCAAAATAGCAACATGATAGTGTATGAGTTCTAGTGGTGGATCTTTGGATGCA 480

QY 4712 TGGAGAATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACTACCGGA 4771
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DB 481 TGGAGAATACCTCCATCAACAAGCTCAGCAATTCCTTTCTTGATCAACTACCGGA 540
QY 4772 TTGGTGCATCTTCAACGCGTTATATCCATTACTAGAAGG 4812
DB 541 TTGGTGCATCTTCAACGCGTTATATCCATTACTAGAAGG 581

RESULT 14
US-09-770-152-196
; Sequence 196, Application US/09770152
; Publication No. US20020040489A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2025US (PARA-014PRV)
; CURRENT APPLICATION NUMBER: US/09/770,152
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,503
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-770-152-196

Query Match          7.6%; Score 577; DB 3; Length 577;
Best Local Similarity 100.0%; Pred. No. 3.7e-250;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4926 CAAGAAATGTGAAGCGGAAGAATGATCAGGATCGGGGTAGGGATGGGATGGAATGA 4985
DB 1 CAAGAAATGTGAAGCGGAAGAATGATCAGGATCGGGGTAGGGATGGGATGGAATGA 60

QY 4986 ATAACCTATCAAGAAACTTTTGGGTAATATCAACATAAACTCAGCAGGAACGAGGAAT 5045
DB 61 ATAACCTATCAAGAAACTTTTGGGTAATATCAACATAAACTCAGCAGGAACGAGGAAT 120

QY 5046 ACACATCATGGGAGGTAACAGTTCTTGGACCGGTTTCACTCCCAACTCAACAGGCC 5105
DB 121 ACACATCATGGGAGGTAACAGTTCTTGGACCGGTTTCACTCCCAACTCAACAGGCC 180

QY 5106 ATCTCTCATTTCTAAGTACTCAGCACTAGTATTTCTTGATGATTTCTTTTGGTGGGT 5165
DB 181 ATCTCTCATTTCTAAGTACTCAGCACTAGTATTTCTTGATGATTTCTTTTGGTGGGT 240

QY 5166 GTACATTCGTCTGTCATGCGAGTTATGCTGAGGAAGATCAAAACCATGCACTATATC 5225
DB 241 GTACATTCGTCTGTCATGCGAGTTATGCTGAGGAAGATCAAAACCATGCACTATATC 300

QY 5226 CAAAGGCTAATTTTGAGGCTCAAGGAAGGATGCTGTTATATAAATCTTTTGTATCTT 5285
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Db      301  CAAAGGCTAATTTGAGGCTCAAAGGAAAGGTATGTTATATAAACTATCTTTTGTATCTT 360
Qy
5286  TTAAAGAATCTTCAAAGTGTGAGTAGTTATTTGTTGGCTTCTGGTGATATTTATGTTT 5345
Db      361  TTAAAGAATCTTCAAAGTGTGAGTAGTTATTTGTTGGCTTCTGGTGATATTTATGTTT 420
Qy      5346  TATTAGAATTTGGTCTTTATATATTTGGCTATATATAGAGGTGCGGTGATATGTAATTT 5405
Db      421  TATTAGAATTTGGTCTTTATATATTTGGCTATATATAGAGGTGCGGTGATATGTAATTT 480
Qy      5406  CAAAGAGTTGATGTTGGAACCTTTTGTGTGTTTCATTGAATTAATCATCGAATTTCTCAATT 5465
Db      481  CAAAGAGTTGATGTTGGAACCTTTTGTGTGTTTCATTGAATTAATCATCGAATTTCTCAATT 540
Qy      5466  TCTTGAGACCCATTATGAGACATTTGAGACATCTATA 5502
Db      541  TCTTGAGACCCATTATGAGACATTTGAGACATCTATA 577

RESULT 15
US-09-938-842A-3563
; Sequence 3563, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3563
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3563

Query Match      4.9%; Score 368; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 1.9e-155;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5763  GAATTATGCACCTAAATTCAGACTAATCCCCCAAATTCAGAAATTTATGTAATTTTGGG 5822
Db      1  GAATTATGCACCTAAATTCAGACTAATCCCCCAAATTCAGAAATTTATGTAATTTTGGG 60
Qy      5823  ATTTAATATTTGTTTCAATATGATGCGCACTAATTTGAAAGACATGGAATG 5882
Db      61  ATTTAATATTTGTTTCAATATGATGCGCACTAATTTGAAAGACATGGAATG 120
Qy      5883  ACTGAAACCATGATATCTCTCAAGTCTCAACCTATGAAGATCATGTAACCAATAGAC 5942
Db      121  ACTGAAACCATGATATCTCTCAAGTCTCAACCTATGAAGATCATGTAACCAATAGAC 180
Qy      5943  TATCATCATGATTAAGTAAATGATGATCTATATAATGATTTTGAACATAGATGTCAT 6002
Db      181  TATCATCATGATTAAGTAAATGATGATCTATATAATGATTTTGAACATAGATGTCAT 240
Qy      6003  TTATCTGGATATAAAGATGGCGTTTAACTACTTTGGCAATTTTGTATATCTTTCTTC 6062
Db      241  TTATCTGGATATAAAGATGGCGTTTAACTACTTTGGCAATTTTGTATATCTTTCTTC 300
Qy      6063  TAATACATATGATCAATACACTTTTGTGTTTTTAAAGAAATTTAAAACTTATTTCAAACAT 6122
Db      301  TAATACATATGATCAATACACTTTTGTGTTTTTAAAGAAATTTAAAACTTATTTCAAACAT 360
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Qy      6123  CGATCACA 6130
Db      361  CGATCACA 368

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Job time : 3574 secs
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